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Title:
Perfect score:
Sequence:
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              you now
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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AR160922
AR160921
AC122438
AC141530
AC141151
AL445257
AL357713
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AC079838
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AX063919
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AR160915 Sequence
AR160922 Sequence
AR160921 Sequence
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AC122438 Mus muscu
AC141153 Rattus no
AC141153 Rattus no
AL1445257 Homo sapi
AL357713 Human DNA
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AC079838 Homo sapi
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ALIGNMENTS

SULT 1 160915 AR160915 AR160915 RSION AR160915 Inhown. Unclassified. 1 (bases 1 to 65) Inhown. Inclassified. 1 (bases 1 to 65) Inhown. Inclassified. Incla	RE ARR DE ARR VE KE	4a 4b	dd VQ		OR FE SE	ARE DE ARE VE SO
GI:16225978 d. to 65; Mukherjee, A. B. and Zhang, Z. mbinant human uteroglobin in treatment of conditions cation/Qualifiers 65 Franism="unknown" ol_type="unassigned DNA" 100.0%; Score 65; DB 6; Length 65; 100.0%; Pred. No. 1.1e-26; vative 0; Mismatches 0; Indels AAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTGCTG AAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTTGCTG AAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTTGCTG AAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTTGCTG AAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTTGCTG AAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTTGCTG AAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTTGCTG AAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTTGCTG AAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTTGCTG	SULT 2 160922/c CUS FINITION CESSION RSION YWORDS URCE			Query Mat Best Loca Matches	FERENCE AUTHORS TITLE JOURNAL ATURES SOURCE	SULT 1 160915 CUS CUS CESSION CESSION RSION YWORDS URCE ORGANISM
F-2001 F-2001	42 bp DNA linear 13 from patent US 6255281.	CGTCC	GATCCATGGAAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTGCTGATGGACACCC	100.0%; Score 65; DB 6; Length 65; 100.0%; Pred. No. 1.1e-26; vative 0; Mismatches 0; Indels 0; Gaps	.B. and Zhang,Z. n uteroglobin in treatment 03-JUL-2001; fiers nown" ssigned DNA"	65 bp DNA from patent US 6255281. GI:16225978

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TITLE
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AC122438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GATCCATGGAAATCTGCCCGTCTTTCCAGCGTGTTATCGAAA 42
Unpublished (2001)
3 (bases 1 to 193659)
McPherson, J.D. and Waterston, R.H.
                                                                                         VanBrunt,A., Creason,K. and Van,Brunt.
The sequence of Mus musculus BAC clone RP24-216M6
Unpublished (2001)
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
l (bases 1 to 193659)
                                                                                                                                                                                                                               Mus musculus BAC clone RP24-216M6 from 5, AC122438 AC122438.2 GI:22296783
                                                                                                                                                                                                                                                                                                                                                                                                                   23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pilon,A.L., Mukherjee,A.B. and Zhang,Z.
Use of recombinant human uteroglobin in treatment of inflammatory
and fibrotic conditions
Patent: US 6255281-A 12 03-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 from patent US 6255281. 
AR160921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pilon,A.L., Mukherjee,A.B. and Zhang,Z. Use of recombinant human uteroglobin in treatment of inflammatory and fibrotic conditions Patent: US 6255281-A 13 03-JUL-2001;
                                               Sequencing of Mus musculus
                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                   Mus musculus (house mouse)
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                                                                            (bases 1 to 193659)
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
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Pred. No. 2.9e-13;
                                                                                                                                                                                                                                                                            193659 bp
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                                                                                                                                                                                                                                                              complete sequence
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                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                  JOURNAL
                                                                                                                                          Submitted (05-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Aug 17, 2002 this sequence version replaced gi:21105899.
                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (17-AUG-2002) Genome Sequencing Center,
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                            Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 193659)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                     (bases 1 to 193659)
                                           Contact: submissions@watson.wustl.edu
                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
Center project name: M_BB0216M06
                                                                  Web site: http://genome.wustl.edu
                       -- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                MO 63108, USA
                                                                                                                                                                                                                                                                                                                                        4444 Forest Park
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeate; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see

SOURCE INFORMATION:

http://genome.wustl.edu

The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org

FEATURES **tRNA** repeat_region repeat_region repeat_region misc_feature repeat_region source NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert of 6385, /note="Likely pseudogene (HMM Sc=-11.21)" /rpt_family="L2" 6139. .6322 Location/ /mol_type="genomic DNA" /db_xref="taxon:10090" /chromosome="5" organism="Mus musculus" rpt_family="MER1_type" product="tRNA-Ser" rpt_family="B2" note="CpG rpt_family="ID" clone_lib="RPCI-24" clone="RP24-216M6" ="CpG_island (%GC=72.2, .4591 Qualifiers o/e=0.86, #CpGs=87)" Sc=33.90 / Sec struct

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/rpt_family="ID"
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9298. .9522
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9048. .9094
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7263. .7443
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_family="tRNA-Ala-GCY_"
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Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
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AC141530.1 GI.28975794
HTG: HTGS PHASE1; HTGS DRAFT.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Praser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Gabregoorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guerara, W., Gunarathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, W., Hollins, B., Howells, S., Hulwe, J., Idebird, D., Jackson, A., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Koyaz, C., Kargathy, S., Kelly, S., Khan, Z., King, L., Koyaz, C., Kargathy, S., Kelly, S., Khan, Z., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R., J., Lu, X., Mangum, A., Mahishawari, M., Mahindarthe, M., Martin, R., Martin, R., Martinez, E., Milosavijevic, A., Miner, G., Minja, B., Montemayor, J., Moore, S., Morgan, M., Morris, S., Manier, G., Minja, B., Montemayor, J., Noore, S., Morgan, M., Morris, S., Nawokelemeh, O., Okwuonu, G., Olarngunsagoon, A., Pal, S., Parke, K., Pasternak, S., Paul, H., Popovic, D., Primus, E., Pal, S., Parke, K., Pasternak, S., Paul, H., Popovic, D., Primus, E., Pal, S., Parke, K., Pasterny, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartbbeyn, A., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartbbeyn, A., Song, X., Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Walter, B., Wang, J., Wang, J., Warren, J., Walter, B., Wang, J., Wang, J., Warren, J., Walter, B., Wang, J., Wang, J., Warren, J., Walter, B., Wang, J., Warren, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Yakub, S., Shith, H.O., Waiss, R., Walsson, J., Shith, H.O., Waiss, R., Smith, D.R., Holt, R.A., Smith, D., Waiss, R., Smith, D.R., Holt, R.A., Smith, D., Waiss, R., Smith, D.R., Holt, R.A., Smith, D.R., Waiss, R., Smith, D.R., Holt, R.A., Smith, D.R., Waiss, R., Smith, D.R., Holt, R., Smith, D.R., Waiss, R., Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 215983) Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                 * NOTE: Stimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/denbank_draft_data.html).

* NOTE: This is a "vorking draft, sequence. It currently

* NOTE: This is a "vorking draft, sequence. It currently

* consists of 47 contigs. The true order of the pieces

is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.
                                                                                                                                                                                                                                                                                                                            Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 200142 bases at least Q40
Consensus quality: 204905 bases at least Q20
Consessus quality: 204905 bases at least Q20
Consessus quality: 208606 bases at least Q20
Estimated insert size: 204516; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: KEFJ
Center clone name: CH230-517N11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: BCM
Web site: http://
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine
1367: contig of 1367 bp in length 1467: gap of unknown length 2579: contig of 1112 bp in length
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ORGANISM
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Anyalebechi, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Anlen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, S., Baden, H., Balderin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bladwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Brawalo, N., Catter, K., Cavazos, I., Ceasar, H., Center, A., Chen, R., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clavelland, C., Cocktell, R., Cox, C., Coyle, M., Cree, A., D. Souza, I., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Dingh, D., Duhh, H., Divya, K., Daya-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C., M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hawes, A., Henderson, N., Hernandez, M., Hollins, B., Howells, S., Hulay, S., Khan, Z., King, L., Kovar, C., Kowis, C., Keally, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Liu, J., Liu, W., Liu, W., Louseged, H., Lozado, R.J., Lu, X., Ma, J., Liu, X., Louseged, H., Lozado, R.J., Lu, X., Ma, J., Lu, X., Ma, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-114H6, WORKING DRAFT SEQUENCE, 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC141151.2 GI:28951124
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/db_xref="taxon:10116"
/clone="CH230-517N11"
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135346: gap of unknown length
142559: contig of 6913 bp in length
142359: gap of unknown length
152944: contig of 10585 bp in length
153044: gap of unknown length
160462: contig of 7418 bp in length
160562: gap of unknown length
168367: gap of unknown length
168367: gap of unknown length
17703: contig of 7705 bp in length
17703: contig of 9336 bp in length
17803: gap of unknown length
17803: gap of unknown length
187092: contig of 9289 bp in length
187192: gap of unknown length
201446: contig of 14254 bp in length
201546: gap of unknown length
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On Mar 14, 2003 this sequence version replaced gi:28894506
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Direct Submission
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                                      Center project Information
Center project name: KEBT
Center clone name: CH230-114H6
Center clone name: Ch231-114H6
Center clone clone
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Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LD8752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 28716 bases at least Q40
Consensus quality: 32676 bases at least Q20
Consensus quality: 32676 bases at least Q20
Insert size: 38296; sum-of-contigs
Insert size: 38296; sum-of-contigs
Ouality coverage: 1.51x in Q20 bases; sum-of-contigs
Quality coverage: 1.51x in Q20 bases; sum-of-contigs
Ouality coverage: 0.97x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (12-UNN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL445257

39596 bp DNA linear HTG 13-JUN-2
Homo sapiens chromosome 1 clone RP5-1175N1, 14 unordered pieces
AL445257
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                                                                                                                                                                                                                                                                                                                                                                         Center project name: dJ1175N1
                                                                                                                                                                                                                                                                                                                                                                                                           Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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HTG; HTGS_PHASE1; HTGS_CANCELLED.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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37110. .39596
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20065. .24184
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29768. .31926
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fragment_chain:1"
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Eragment_chain:1"
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/mol type="genomic DNA"
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                                                                                                                                                                               'note="assembly_fragment:00532"
                                                                                                                                                                                                                                                                       note="assembly_fragment:00489"
                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment:00304"
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Fragment_chain:2"
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ragment_chain:2"
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/db_xref="taxon:9606"
/chromosome="1"
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14756: gap of 100 bp
17428: contig of 2672 bp in length
19528: gap of 100 bp
1964: contig of 2436 bp in length
20064: gap of 100 bp
24184: contig of 4120 bp in length
24284: gap of 100 bp
26468: contig of 2184 bp in length
26468: gap of 100 bp
29567: gap of 100 bp
29567: gap of 100 bp
39267: gap of 200 bp in length
34705: contig of 2679 bp in length
34705: gap of 100 bp
34706: gap of 100 bp
                                                                                       27.7%; Score 18; DB 2; Length 39596; 100.0%; Pred. No. 20;
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP there, //www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human thus; //www.sanger.ac.uk/HGP/Chr1

RP11-3J23 is from the library RPCI-11.1 constructed by the group of Pleter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9888 ATCCATGGAAATCTGCCC 9905
                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is not the entire insert of clone Rp11-3/23 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone Rp4-63318 is at 103414 in this sequence. The true right end of clone Rp5-1115A15 is at 100 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On or before May 15, 20 gi:7283183, gi:13160267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 103513)
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Human DNA sequence from clone RPI1-3J23 on chromosome 1, complete
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AL357713 AC021953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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VECTOR: pBACe3.6
                                                                                                                                                                                                                                  /clone
                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
                          'note="AluSx repeat: matches 3. .300 of consensus"
                                                                      note="AluJo repeat: matches 3.
                                                                                                                  'note="146 copies 2 mer aa 55% conserved"
                                                                                                                                                                                                          'note="36 copies 2 mer aa 65% conserved"
                                                                                                                                                                                                                                                                         clone="RP11-3J23"
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LMFLCHR36_11/c
WPCOMMENT
Sequence split into 36 fragments LOCUS LMFLCHR36 Accession AL499624

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RESULT 9
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Matches 18; Conservative
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                                                                   80412 ATCCATGGAAATCTGCCC 80429
                                                                                              2 ATCCATGGAAATCTGCCC 19
                                                                                                                                                                                                                                                    /note="Alux repeat: matches 1. .289 of consensus" 52994 . .53120 /note="L2 repeat: matches 2565. .2703 of consensus" 53182 . .53488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25427. ,25721
/note="AluJo repeat: matches 1. .299 of consensus".
26005. .26137
                                                                                                                                                                                                                                                                                                                                                                                                                                     note="26 copies 2 mer ac 84% conserved"
0629. .50680
                                                                                                                                                                                                                                                                                                                                                                                                            note="13 copies 4 mer caca 84% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="Aludo repeat: matches 1. .282 of consensus" 0626. .50677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="AluSq/x repeat: matches 1. .136 of consensus"
6138. .26443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluSx repeat: matches 1. .307 of consensus" 7061. .27268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="FRAM repeat: matches 1. .160 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="AluY repeat: matches 3. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MER94 repeat: matches 2..100 of consensus"
)688..39711
note="12 copies 2 mer aa 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 16. .223 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ote="11 copies 4 mer cata 86% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ote="L2 repeat: matches 2666. .2749 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ote="Alusx repeat: matches 1. .309 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ote="AluJb repeat: matches 3. .209 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ote="FLAM_C repeat: matches 1. .123 of consensus"
618. .44082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ote="Alusq repeat: matches 9. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ote="AluSg repeat: matches 1. .305 of consensus"
854. .28032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107. .47918
Ste="AluJo/FRAM repeat: matches 169. .280 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ote="AluSx repeat: matches 44. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ote="LTR19A repeat: matches 1. .486 of consensus"
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365. .42459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ote="L2 repeat: matches 2571. .2701 of consensus"
                                                                                                                                                        27.7%; Score 18; DB 9; Length 103513; 100.0%; Pred. No. 19; Indels 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                   e="AluJb repeat: matches 1. .306 of consensus"
.7. .52235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e="21 copies 2 mer ac 78% conserved"
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LMFLCHR36_29 29
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                                                                                                                                                                                                                                                                                                                                                              66513
                    2 (bases 1 to 156481)
Waterston, R.H.
Direct Submission
Submitted (12-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Apr 1, 2001 this semisor .....
                                                                                                                                                                                                                                                                                                                                                                                14 CTGCCCGTCTTTCCAGCG 31
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                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 156481)
Waterston, R.H.
                                                                                                                                                                                                                                                                AC079838 156481 bp DNA linear HTG 01 Homo sapiens chromosome 2 clone RP11-257N14, WORKING DRAFT SEQUENCE, 2 unordered pieces.
                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                               The sequence of Homo sapiens clone
                                                                                                                                                                                                                                       AC079838.3 GI:13493151
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100.0%; Pre
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                                                                                                      Homo sapiens
           99063792
                                                                                                                                              AC007098.4 GI:11038585
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                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP11-257N14"
1. .6178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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100.0%; F1
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ACUU7U98 157650 bp DNA
Homo sapiens BAC clone RP11-443F16 from 2,
AC007098
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 157650)
Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 6178: contig of 6178 bp in length
6179 6278: gap of unknown length
6279 156481: contig of 150203 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector_side:right"
6279. _156481
/note="assembly_name:Contig8
clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig7
                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.7%; Score 18; DB 2; Length 156481; 100.0%; Pred. No. 18;
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                                                                                                                                                            source
                                                                                                                                                                                             The clone sequenced to the right is RP11-511111, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-443F16, actual end is at base position 157456 of RP11-443F16.
                                                                                                                                                                                                                                                                                                                                  The RPCT-11 human BAC library was made from the blood of one male donor, as described by Gsoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repears; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence, see http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAPPING INFORMATION:
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                                                                                                                                                                                                                                                                   NEIGHBORING SEQUENCE INFORMATION:
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Kallcki,J., Johnson,D. and Harris,A.
Fig. sequence of Homo sapiens BAC clone RP11-443F16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://genome.wustl.edu/gscContact: sapiens@watson.wustl.edu
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    /clone_lib="RPCI-11"
                                             map="2"
                                                                     chromosome="2"
                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                               organism="Homo sapiens"
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                                                                BST Z21249 (NID:g27992)"
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Direct Submission
Submitted (21-MAY-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Sylvan Harbor, NY 11724, USA
On Oct 7, 2000 this sequence version replaced gi:9972279.
* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 167711)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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Best Local :
                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 CCCTGCTGATGGACACCC 60
                                                                                                                                                                                                                                                                    Submitted (04-JUN-2003) Pediatrics, Columbus Children's Research Institute and The Ohio State University, 700 Children's Drive,
                                                                                                                                                                                                                                                                                                        2 (bases 1 to 191854)
Munson,R.S. Jr., Ray,W.C., Mahairas,G., Sabo,P., Mungur,R.,
Johnson,L., Nguyen,D., Wang,J., Forst,C. and Hood,L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 191854)
Munson,R.S. Jr., Ray,W.C., Mahairas,G., Sabo,P., Mungur,R., Johnson,L., Nguyen,D., Wang,J., Forst,C. and Hood,L. The Complete Genome Sequence of Haemophilus ducreyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus ducreyi 35000HP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE017156 191854 bp DNA linear BCT 15-AUG-20 Haemophilus ducreyi strain 35000HP section 6 of 6 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome.
                                                                                                                                                                                                                                                      Columbus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE017156.1 GI:33149035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE017156 AE017143
                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved
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142299
157946
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160828
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                                                                  /locus_tag="HD1803"
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                                                                                                                        /db_xref="taxon:233412"
complement(142. .2073)
                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                 organism="Haemophilus ducrey1 35000HP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="NH0443B15a"
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160827: contig of 2782 bp in length
160927: gap of unknown length
163434: contig of 2507 bp in length
163534: gap of unknown length
165854: contig of 2320 bp
167911: contig of 1757 bp in length
167911: contig of 1757 bp in length
                                                                                                                                                                                                                      .19185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142198: contig of 142198 bp in length 142298: gap of unknown length 157945: contig of 15647 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.7%; Score 18; DB 2; 100.0%; Pred. No. 18; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
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                                                                             complement (5519. .6817)
                                                                                                                                                                                                           complement (5519. .6817)
                                                                                                                                                                                                                                         KDVVAVEATSALTEKDIILDIRSPEEMDEKPLVLAQAQVIELPFYKLSTQFAHLDQSK
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/locus_tag="I
                                      gene="purA"
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (20-DEC-2002) Applied Microbiology, Biozentrum,
Universitaet Basel, Klingelbergstrasse 50-70, Basel CH-4056,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Eremothecium.

1 (bases 1 to 306790)
Dietrich,F.S., Voegeli,S., Brachat,S., Lerch,A., Gates,K., Steiner,S., Mohr,C., Pohlmann,R., Luedi,P., Choi,S., Wing,R.A., Flavier,A., Gaffney,T.D. and Philippsen,P.
Flavier,A., Gaffney,T.D. and Philippsen,P.
The Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome Science 304 (5668), 304-307 (2004)
                                                                                                                                                                                                                                                                                                                 This is low coverage sequence generated to identify the complete set of genes and the gene order on this chromosome. Regions of low quality are identified. Before doing extensive work on any gene identified here the sequence should be confirmed.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eremothecium gossypii (Ashbya gossypii)
Eremothecium gossypii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachat, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE016888 AE016816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Philippsen, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE016888.1 GI:44981618
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LGAIIVSIPSBVLGGAGLMMFAMIIAAGIQMLDKYBERKKNGLIIAISIGCGLAVTTR
PELLDKLPNFFKEVFGSGITVGSVLALLLNLILPEDKH"
COMPLement (11033. ..12871)
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                                                                                                                                                                       /db_xref="ATCC:10895"
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                                                                                                                                                    omosome="III"
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GIYISNAQNENSPVGEIVLGGYNTQKFKGDIKMLPVLRKAFWETDLSAFKVUNFALDV
                                                                                                                                                                                                                                                      YPL154C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      <3039. .>4265
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YPL154C (PEP4); tandem gene duplication in Ashbya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1102. .>2283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="region of low quality - less than
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                                                                                                                                                                                                                                                                                                                                                                          'locus_tag="ACR144W"
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\LKLSARDYVMQLGRNTCILAVSGNSRVTGEVILGDTFLRRYYTIXNFGDNTIGVASA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xref="taxon:33169"
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                                                                                                                                                                                                                                                   (PEP4); tandem gene duplication in Ashbya
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VTVGDDNI PLENYGAAIDSGTSLLTFSSELFNQFISKLSGVTKDRGGNVVVDCANKQT
APPLTFGFGGKKESISGEDYIISVFGQSARCMPAIVQLDIDSAGKVAIIGDVFLRRYY
SIYDFGNNAVGLATAV"
                                                                                                                                                         lcfwgeafynfdaaspansgerlaarloeahdlyg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(<8145...>9080)
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complement(8145...9080)
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GTDESSRYLRHLLTNEYEVTPBIAVVDLSKHRYSGDLQRYIREHKLHGDLFQLTENTP
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                                                                    /locus_tag="ACR148W"
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/locus_tag="ACR147C"
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YPL156C (PRM4)"
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product="ACR146Wp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-NOV 2002) Submitted on behalf of the Nitrosomonas genome consortium, the DOE Joint Genome Enstitute, Production Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA, and the Genome Analysis Group, Oak Ridge National Laboratory, USA, Commerce Park Drive, Oak Ridge, TN 37831, USA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nitrosomonas europaea ATCC 19718
Nitrosomonas europaea ATCC 19718
Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313050 bp DNA linear BCT 23-APR-2
Nitrosomonas europaea ATCC 19718, complete genome; segment 2/10.
EX321857 AL954747
EX321857.1 GI:30138174
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Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautotroph Nitrosomonas europaea
J. Bacteriol. 185 (9), 2759-2773 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         larimerfw@ornl
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complement (885. .1253)
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complement (885. .1253)
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain="ATCC 19718"
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complement (1253. .1660)
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/function="COGs COG3293"
                                                              /locus tag="NB0274"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="cyc"
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LAAYYSOQKPQDGTASDASLVETGKKLYQGGNLENSIPACSSCHSPNGQGIPPHYPRI
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QIEQLKKSGISKLHIQENADSYWHNLSLALLPDDSDVAALVEELKGKGVERINDSEQ
VLEQFEFDIRNPTEQITESVRQLAQQFPETKLEVTECSRL"
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/protein_id="CAD84184.1"
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TGALKKTVFKLSVNHBGAGLPKFTWSRQNPEPR"
complement (1853. . .2488)
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Sg

CDS

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LDLEKLGERTIQMDCDVIQADGGTRTASITGAFVALYDAIDYLRAERMISQNPIRDHV
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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Gapop_60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
geneseqn2003cs:*
geneseqn2003ds:*
geneseqn2004s:*
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geneseqn2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
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ID SABZ5
XX ABZ5
XX ABZ5
XX BAZ5
XX Huma
XX Huma
DE Huma
XX Homc
OS Synt
XX Synt
XX BAC1
PN W020
PN 28-APR-2003 ABZ58370; ABZ58370 standard; DNA; 65 Human uteroglobin synthetic gene oligonucleotide 1. (first entry)

Human; uteroglobin; respiratory distress; antiinflammatory; antifibrotic; antiinflammatory; antiasthmatic; nephrotropic; antirheumatic; antiarthritic; ss. Homo sapiens. Synthetic.

16-JAN-2003. WO2003003979-A2.

02-JUL-2001; 2001US-00898616. 02-JUL-2002; 2002WO-US020836.

(CLAR-) CLARAGEN INC

Pilon AL, Welch RE;

WPI; 2003-221527/21.

Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic gene which codes for human uteroglobin.

Claim 1; Page 33; 127pp; English.

The present sequence is that of oligonucleotide 1, which was used in the construction of a synthetic gene for the production of human uteroglobin (hUg) in bacteria. Oligonucleotides 1-4 (see ABZ58370-73) were used to assemble the coding strand and oligonucleotides 5-8 (see ABZ58374-77) the complementary strand. The gene was assembled by annealing and ligation of the oligonucleotides. Because mature native hUg has glutanic acid at its N-terminus, an initiator methionine was added to the N-terminus, and

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Best Local :
   The invention relates to a bacterial expression system for the production of recombinant human uteroglobin (rhUG), comprising a synthetic gene or human cDNA sequence which codes for human UG, constructed from the oligonucleotides appearing as ADL27626-ADL27629, and which further comprises Met-Ala-Ala at the N-terminus of the sequence. Also included are producing an rhUG master cell bank (comprising inoculating a suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon usage was optimised for expression in bacteria. In an example from the invention, the synthetic gene was cloned into plasmid pCG12 (see AB5258378) and recombinant hUG (see AB57259) was produced in Escherichia coli strain CG12. The invention relates generally to the production of recombinant hUG by bacterial expression, protein purification and scaled-up production according to current good manufacturing practices. The recombinant hUG is useful for the treatment of inflammatory and fibrotic
                                                                                                                                                                Bacterial expression system for production of recombinant human uteroglobin comprising synthetic gene or human cDNA sequence wh for human uteroglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ss; recombinant human uteroglobin; rhUG; bacterial expression system; rhUG master cell bank; rhUG research seed bank; anti-inflammatory; secretory phospholipase A 2; fibronectin; respiratory distress; inflammation; fibrotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conditions, such as neonatal respiratory distress syndrome and bronchopulmonary dysplasia. It may also be used to treat conditions associated with elevated phospholipase A2 levels such as pancreatitis,
                                                                                                                             Claim 1; SEQ ID NO 1; 64pp; English.
                                                                                                                                                                                                                                         WPI; 2004-051527/05.
                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1997;
02-JUL-2001;
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                                                                                                                                                                                                                                                                                                             (PILO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant human uteroglobin, rhUG, coding oligonucleotide
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                                                                                                                                                                                                                                                                              Welch RW;
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                                                                                                                                                                                                                                                                                                                                                                   2001US-00898616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      97US-00864357
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                     or human cDNA sequence which codes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 65
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conscious times a large scale fermenter with the incovalum formed from the cc step (c) to form a fermentation culture, incubating the fermentation culture within the large scale fermenter, incubating the fermentation culture within the large scale fermenter, adding an induction agent to the above fermentation culture), purifying rhNG, determining the potency of rNUG in a sample, measuring in vitro anti-inflammatory effect arising crom inhibition or blocking of secretory phospholipase A 2 enzymes by cc from inhibition or vitro binding of rNUG to fibromectin, determining the potency cc purity of rNUG, and a pharmaceutical composition comprising a purified cr hVG and a carrier or diluent. The bacterial expression system is useful cod drug substance. rNuG is safe to administer to a patient in respiratory cc distress. The rNUG is useful for treating inflammation and fibrotic construct the synthetic rNUG gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  incubating broth with an aliquot portion of a rhUG research seed bank to form a bacterial culture, incubating the bacterial culture, adding a cryopreservative to the bacterial culture to form a cryopreserved solution, transferring a portion of the cryopreserved solution to a cryovial and storing the cryovial at a temperature below -60 degrees C), expressing rhUG (comprising providing a production seed cell bank culture comprising an expression rhUG, incoulating a broth medium with the production seed cell bank culture to form an broth medium with the production seed cell bank culture to form an brothum, incubating the bacterial culture formed in step (b),
Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic
                                                    WPI; 2003-221527/21.
                                                                                    Pilon AL,
                                                                                                                                                         02-JUL-2001; 2001US-00898616
                                                                                                                                                                                         02-JUL-2002; 2002WO-US020836.
                                                                                                                                                                                                                                                               WO2003003979-A2
                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                   antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                    Human; uteroglobin;
antiinflammatory; as
                                                                                                                                                                                                                                                                                                                                                                                                                   Human uteroglobin synthetic gene oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ58376 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 65 BP; 13
                                                                                                                                                                                                                           16-JAN-2003
                                                                                                                        (CLAR-) CLARAGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCCATGGAAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTGCTGATGGACACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATCCATGGAAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTGCTGATGGACACCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTCC
                                                                                      Welch RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                    antiasthmatic; nephrotropic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 22 C; 14 G; 16 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                   respiratory distress; antiinflammatory; antifibrotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 65;
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RESULT 4
ABZ58377/c
ID ABZ583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                construction of a synthetic gene for the production of human uteroglobin (hUG) in bacteria, Oligonucleotides 1-4 (see ABZS8370-73) were used to assemble the coding strand and oligonucleotides 5-8 (see ABZS8374-77) the complementary strand. The gene was assembled by annealing and ligation of the oligonucleotides. Because matture native hUG has glutamic acid at its CC whereinus, an initiator methionine was added to the N-terminus, and code usage was optimised for expression in bacteria. In an example from the invention, the synthetic gene was cloned into plasmid pcG12 (see ABZS8378) and recombinant hUG (see ABZC8378) was produced in Escherichia CC coli strain CG12. The invention relates generally to the production of recombinant hUG by bacterial expression, protein purification and scaled-cup production according to current good manufacturing practices. The recombinant hUG is useful for the treatment of inflammatory and fibrotic conditions, such as neonatal respiratory distress syndrome and conditions, such as neonatal respiratory distress syndrome and conditions as accorded with elevated phospholipase A2 Levels such as pancreatitis, accurate renal failure, rheumatcid arthritis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; uteroglobin; respiratory distress; antiinflammatory; antifibrotic; antiinflammatory; antiasthmatic; nephrotropic; antirheumatic; antiarthritic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 60 BP; 12 A; 14 C; 22 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of oligonucleotide 7, which was used in the construction of a synthetic gene for the production of human uteroglobin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene which codes for human uteroglobin.
gene which
                     Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic
                                                                                                            WPI; 2003-221527/21.
                                                                                                                                                                      Pilon AL,
                                                                                                                                                                                                                                                                                  02-JUL-2001; 2001US-00898616
                                                                                                                                                                                                                                                                                                                                          02-JUL-2002; 2002WO-US020836.
                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003003979-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human uteroglobin synthetic gene oligonucleotide 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-2003
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                                                                                                                                                                                                                        (CLAR-) CLARAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 CCCTGCTGATGGACACCCCGTCC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                   Welch RE;
codes for human uteroglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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The present sequence is that of oligonucleotide 8, which was used in the construction of a synthetic gene for the production of human uteroglobin

The invention relates to a bacterial expression system for the production of recombinant human uteroglobin (rhig), comprising a synthetic gene or human cDNA sequence which codes for human UG, constructed from the oligonuclectides appearing as ADI27628-ADI27629, and which further comprises Met-Ala-Ala at the N-terminus of the sequence. Also included

Example 1; SEQ ID NO 8; 64pp; English.

for human uteroglobin.

Example 1; Page 33; 127pp; English

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RESULT 5
ADL27633/c
ID ADL276
XX ADL276
XX ADL276
XX ADL276
XX Human;
XW Human;
XW Human;
XW Fibron
XX Homo 8
OS Synthe
XX US2003
XX US2003
XX O6-NOV
PF 02-JUL
XX (PILO/
PA (WELC/
YA (PILO/
PA (WELC/
YA (WE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                              Bacterial expression system for production of recombinant human uteroglobin comprising synthetic gene or human cDNA sequence which codes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; recombinant human uteroglobin; rhUG; hacterial expression system; rhUG master cell bank; bacterial expression system; rhUG master cell bank; rhUG research seed bank; anti-inflammatory; secretory phospholipase A 2; fibronectin; respiratory distress; inflammation; fibrotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-051527/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pilon AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1997; 97US-00864357 02-JUL-2001; 2001US-00898616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2002; 2002US-00187498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003207795-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant human uteroglobin, rhWG, non-coding oligonucleotide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PILO/) PILON A L. (WELC/) WELCH R W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Welch RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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for human uteroglobin

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ID ADL27632 standard; DNA; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC are producing an rhUG master cell bank (comprising inoculating a suitable CC incubating broth with an alignot portion of a rhUG research seed bank to CC form a bacterial culture, incubating the bacterial culture, adding a CC cryopreservative to the bacterial culture to form a cryopreserved CC comprising a portion of the cryopreserved solution, transferring a portion of the cryopreserved solution to a CC cryovial and storing the cryovial at a temperature below -60 degrees C), CC expressing rhUG (comprising providing a production seed cell bank culture CC comprising an expression vector capable of expressing rhUG, inoculating a broth medium with the production seed cell bank culture to form an incubating the bacterial culture formed in step (b), CC inoculating a large scale fermenter with the inoculam formed from the CC inoculating a large scale fermenter with the inoculam formed from the CC the fermentation culture, incubating the fermentation culture within the large scale fermenter, adding an induction agent to culture within the large scale fermenter, adding an induction agent to comprise the culture to induce the expression of rhUG and harvesting CC the above fermentation culture), purifying rhUG, determining the potency of rhUG, measuring in vitro binding of rhUG anti-inflammatory effect arising CC rhUG and a carrier or blocking of secretory phospholipase A z enzymes by curity of rhUG, and a pharmaceutical composition comprising a purified CC wild and a carrier or diluent. The bacterial expression system is useful CC discress. The present sequence is a non-coding strand oligonucleotide used to construct the synthetic rhUG gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
Bacterial expression system for production of recombinant human uteroglobin comprising synthetic gene or human cDNA sequence which codes
                                                               WPI; 2004-051527/05
                                                                                                                                                                                                            28-MAY-1997; 97US-00864357.
02-JUL-2001; 2001US-00898616.
                                                                                                                                                                                                                                                                            02-JUL-2002; 2002US-00187498.
                                                                                                                                                                                                                                                                                                                     06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                              US2003207795-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; recombinant human uteroglobin; rhUG;
bacterial expression system; rhUG master cell bank;
rhUG research seed bank; anti-inflammatory; secretory phospholipase A 2;
fibronectin; respiratory distress; inflammation; fibrotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 60 BP; 12 A; 14 C; 22 G; 12 T; 0 U; 0 Other;
                                                                                                      Pilon AL,
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant human uteroglobin, rhUG, non-coding oligonucleotide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 CCCTGCTGATGGACACCCCGTCC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                             PILON A L.
WELCH R W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                        Welch RW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.4%; Score 23; DB 12; Length 60; 100.0%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                  EXEXPONDADADADADADADADADADADADADADADADADADA
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                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60 BP; 12 A; 14 C; 22 G; 12 T; 0 U; 0 Other;
ABK10937;
                                              ABK10937 standard; DNA; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a bacterial expression system for the production of recombinant human uteroglobin (rhUG), comprising a synthetic gene or human CDNA sequence which codes for human UG, constructed from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 7; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    to construct the synthetic rhug gene.
                                                                                                                                                                                                                                     43 CCCTGCTGATGGACACCCCGTCC 65
                                                                                                                                                                                    60 CCCTGCTGATGGACACCCCGTCC 38
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                              35.4%; 5.
100.0%; Prr
                                                                                                                                                                                                                                                                                                                    Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                    DB 12; Length 60; 0.014;
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ABK10937

ABK10937

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AC ABK1

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DT 20-M

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KW Hyma

KW EF 1

KW IRAP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000; 2000KR-00053613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KR2001069245-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; retrovirus vector; elongation factor 1-alpha; gene therapy;
EF lalpha; Murine Leukaemia Virus; MLV; multi-cloning site; MCS; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer IRAPS relating to modified retroviral vector invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRAP5; ss.
                                                                                                                                     VIROMED LTD.
      Lee JT,
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             Yoo SS;
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RESULT 8
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Best Local S
Matches 17
The invention relates to a novel retroviral vector, derived from a murin leukaemia virus (MLV) vector, which lacks viral coding sequences but which includes: (i) part of the non-coding sequence (I) of elongation factor 1 alpha (BF1a), as heterologous, gene-derived sequence, inserted upstream of the multiple cloning site, and (ii) a mutation, downstream of the splice acceptor, within (I). The retroviral vectors are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; elongation factor 1-alpha; retroviral vector; EF1a; murine leukaemia virus vector; MLV; elongation factor 1 alpha; gene therapy; interleukin-1 receptor antagonist; IL-1ra; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-coding sequences derived from the human elongation factor I-alpha gene (EF lalpha, bases +773 to +1006), which can be effectively used in gene therapy due to it's high stability and expression. The Murine Leukaemia Virus (MIV)-derived retrovirus vector is modified by complete removal of the gag, env and pol genes to improve gene expression and virus productability. It is also modified to contain the non-coding portion of the EF lalpha gene upstream of a multi-cloning site (MCS). The present sequence represents a primer used in the methods of the present
                                                                                                                                                                                                                                                                                                                      08-SEP-2000; 2000KR-00053613.
                                                                                                                                                                                                                                                                                                                                                       08-SEP-2001; 2001WO-KR001515.
                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200220810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK47610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a retrovirus vector containing modified non-coding sequences derived from the human elongation factor 1-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin-1 receptor antagonist (IL-1ra), PCR primer IRAP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 31; 32pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retroviral vectors useful in gene therapy, containing no viral coding sequences but which includes a human elongation factor 1 alpha non-coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-065240/09
                                                                                                                  Example 5; Page 45; 47pp; English.
                                                                                                                                                                     sequences
                                                                                                                                                                                                                                                                                       (VIRO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCCATGGAAATCTGC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCCATGGAAATCTGC 18
                                                                                                                                                                   l vectors useful in gene therapy, containing no viral coding but which includes a human elongation factor 1 alpha non-coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 9 A; 11 C; 10 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                      Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antagonist; IL-1ra; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 36;
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AAH66339/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynuclectides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1999; 99JP-00377484
07-APR-2000; 2000JP-00159162
03-AUG-2000; 2000JP-00280988
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                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID NO 1374; 246pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coryneform bacterium; amino acid organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C glutamicum coding sequence fragment SEQ ID NO: 1374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2000; 2000EP-00127688
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Senoh A, Ikeda M,
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da M, Ozaki
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene.
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sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids acids, vitamins, saccharides and organic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office

The present invention provides a number of nucleotide and protein

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RESULT 10
AAF71853/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purime base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF71853;
                                                                                                                                                                                                                                            08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200100843-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF71853 standard; DNA; 1113 BP
                                                                                                                                        09-JUL-1999
                                                                                                                                                              09-JUL-1999
                                                                                                                                                                         08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                       99DE-01030476.
99US-0142101P.
99DE-01031415.
99DE-01031418.
99DE-01031419.
                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0141031P
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Pred. No. 26;
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    RESULT 11
AAS96115/c
ID AAS961:
XX AAS961:
XX AAS961:
XX AAS961:
XX BE C. gluv
XX Metabo
XX Metabo
XX Metabo
XX Corynel
XX Corynel
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XX WO2001
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XX WO2001
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Best Local Similarity
Marches 17; Conserva
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27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
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03-SEP-1999;
03-SEP-1999;
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03-SEP-1999;
03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                            AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (NP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, data, carabohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes
                                                                    Metabolic pathway protein; MP; lysine biosynthesis pathway; methionine biosynthesis pathway; large-scale production of Corynebacterium diphtheriae; diphtheria; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases.
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31-AUG-1999;
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31-AUG-1999,
                            WO200166573-A2
                                                 Corynebacterium glutamicum
                                                                                                                                            26-FEB-2002
                                                                                                                                                                                       AAS96115 standard; DNA; 1113 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BADI ) BASF
                                                                                                                   glutamicum gene #40 encoding metabolic pathway protein.
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DB; AAB79734.
                                                                                                                                                                                                                                                 788
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99DE-01042124.
99DE-01042129.
2000US-0187970P.
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99DE-01040764.
99DE-01040765.
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100.0%; F1
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Gaps

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chemical;

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RESULT 12
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Best Local S
Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterim and Brevibacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2
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23-JUN-2000; 2000US-00606740.
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                                                                                                                Drmanac RT,
                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #10764.
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                                                                                                                                                                      (HYSE-) HYSEQ INC.
                         2001-639362/73
DB; ABG10773.
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                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Pred. No.
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26;
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98 AAACCCTGCTGATGGAC 114

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CC sequences: (I) is useful as hybridisation probes, polymerase chain (CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed (I) is useful in gene therapy techniques to restore mormal (CC sethvity of (II) or to treat disease states involving (II) is (II) or to treat disease states involving (II) is (III) in (III) is (III) is (III) is (III) is (III) is (III) is (III) in (III) is (III) is (III) is (III) is (III) is (III) is (III) in (III) is (III) in (III) is (III) in (III) in (III) is (III) in (I
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                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutations
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Sequence 2055 BP; 469 A; 581 C; 604 G; 401 T; 0 U; 0 Other;

Ş Query Match Best Local : Matches 40 AAACCCTGCTGATGGAC 56 Similarity Conservative 26.2%; 0 Score 17; ; Pred. No. Mismatches DB 5; 0, Length 2055; Indels 0, Gaps 0

RESULT 13 ACA43988 Prokaryotic essential gene #25645. ACA43988; ACA43988 standard; DNA; 2877 BP. 19-JUN-2003 (first entry)

Antisense; ds; prokaryotic essential gene; cell proliferation; design;

Pseudomonas putida.

WO200277183-A2

03-OCT-2002 21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC

Wang L, Wall D, WPI; 2003-029926/02 Zamudio C, Trawick JD, Malone Carr G ์ ลู๊ Haselbeck R, Yamamoto Ohlsen Forsyth Z E Zyskind JW; Xu HH;

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AAS544085
ID AAS54
XX AAS54
AC AAS54
AC AAS64
XX 13-FE
XX Antis
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                                                                                                                                                                                                                                                                                                                                                                                Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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        21-MAR-2000; 2000US-0191078P
                                                                                 21-MAR-2001; 2001WO-US009180.
                                                                                                                                                           27-SEP-2001.
                                                                                                                                                                                                                                         WO200170955-A2
                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa DNA for cellular proliferation protein #216.
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100.0%; F1.
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26-MAY-2000; 2000US-0207727P.

23-OCT-2000; 2000US-0242578P.

27-NOV-2000; 2000US-0253625P.

22-DEC-2000; 2000US-0257931P.

16-FEB-2001; 2001US-0269308P.
21-MAR-2001; 2001US-00815242
06-SEP-2001; 2001US-00948993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2892 BP; 594 A; 1063 C; 824 G; 411 T; 0 U; 0 Other;
                                                    21-MAR-2002; 2002WO-US009107
                                                                                        03-OCT-2002
                                                                                                                           WO200277183-A2
                                                                                                                                                            Pseudomonas aeruģinosa
                                                                                                                                                                                               Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
                                                                                                                                                                                                                                                   Prokaryotic essential gene #23856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibiotics, comprise sequences of antisense nucleic
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Xu HH;
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100.0%; Pred. No.
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Matches 17; Conserv
                                                                                                                                                                                                                                 Sequence 2892 BP; 594 A; 1063 C; 824 G; 411 T;
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08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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P-PSDB; ABU38329.
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Trawick JD,
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                                                                                                             Conservative
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                                                                                                                                       26.2%; Score 17; DB 8; 100.0%; Pred. No. 26;
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Yamamoto R,
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Forsyth RA,
                                                                                                                                                                    Length 2892;
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Xu HH;
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Search completed: December 22, 2004, 22:44:07 Job time: 234.662 secs

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Maximum DB seq length: 200000000
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US-08-864-357F-13
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US-09-252-991A-3091
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US-09-489-039A-3704
US-09-489-039A-3704
US-09-489-039A-3704
US-09-566-921-61
US-09-566-921-61
US-09-566-921-61
US-09-563-99C-11687
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US-09-614-124B-1590
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US-09-614-124B-273
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Sequence 61, Appl
Sequence 122, Appl
Sequence 1590, Ap
Sequence 273, App
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Sequence 12, Appl
Sequence 2879, Ap
Sequence 3091, Ap
Sequence 1155, Ap
Sequence 3704, Ap
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Sequence 481,
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US-08-916-421B-1	US-09-453-702B-137	US-08-311-731A-131	US-09-453-702B-79	US-09-453-702B-252	US-09-453-7028-7	US-08-406-030A-23	US-09-799-451-726	US-08-717-294-42	US-09-863-040-3	US-09-189-462-3	US-09-799-451-152	US-09-375-318-35	US-09-489-039A-2526	US-09-566-921-117	US-09-248-796A-4823	US-09-658-824-342	US-U9-658-824-273
Sequence 1, Appli	Sequence 137, App	Sequence 131, App	Sequence 79, Appl	Sequence 252, App	Sequence 7, Appli	Sequence 23, Appl	72	Sequence 42, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 152, App	Sequence 35, Appl	Sequence 2526, Ap	Sequence 117, App	Sequence 4823, Ap	Sequence 342, App	sequence 2/3, App

ALIGNMENTS

RESULT 1

US-08-864-357F-6

Sequence 6, Application US/08864357F Patent No. 6255281 GENERAL INFORMATION:

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FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 65
CERGINES: ORGANISM: artificial
APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Huma
TITLE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 42
TYPE: DNA
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; OTHER INFORMATION: primer sequence
US-08-864-357F-6
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                                                                                                                                                                                                     ; Sequence 13, Application US/08864357F Patent No. 6255281 ; GENERAL INFORMATION: APPLICANT: Claragen, Inc. & NIH
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Best Local (
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TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammator
TITLE OF INVENTION: Fibrotic Conditions
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Use of Recombinant Human Uteroglobin in Treatment of Inflammato
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100.0%; Pred. No. 1.3e-26
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PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 198-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 2879

LENGTH: 2997

TYPE: PRIOR NUMBER: US 60/094,190
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; OTHER INFORMATION: primer sequence
US-08-864-357F-13
                                                                                                                                                                                             US-09-252-991A-2879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: primer sequence US-08-864-357F-12
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SEQ ID NO 12
LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2879, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08864357F Patent No. 625281 GENERAL INFORMATION: APPLICANT: Claragen, Inc. & NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                       Matches
                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammato
TITLE OF INVENTION: Fibrotic Conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: artificial
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                                                                                                                            Local
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                                                                                                       l Similarity
17; Conser
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                                              CCTGCTGATGGACACCC 60
                  CCTGCTGATGGACACCC 796
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                                                                                                  26.2%; Score 17; DB 4; ilarity 100.0%; Pred. No. 3.1; Conservative 0; Mismatches
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US-09-252-991A-3091/c
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DOUBLENOUS OF APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 1155
LENGTH: 894
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APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PRIOR DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
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Patent No. 6551795
                                                                                                                                                                                        Sequence 3704, Application US/09489039A Patent No. 6610836
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APPLICANT: GREY Breton et.al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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APPLICATION 435

CLASSIFICATION 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14.MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5047
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3704
LENGTH: 1119
                                                                       Matches
                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBL
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILLING DATE: 09-MAY-1997
CINSETERATION AGE
                                                                                                                                                        STRANDEDNESS: sin TOPOLOGY: linear
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                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
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1011 TCCATGGAAATCTGCC 1026
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                                                                     16;
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                           3 TCCATGGAAATCTGCC 18
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                                                                                      Similarity
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                                                                 24.6%; Score 16; DB 3; Length 1155; 100.0%; Pred. No. 11; ative 0; Mismatches 0; Indels
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100.0%; Pred. No.
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US-09-023-655-481
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US-09-023-655-481/c
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                Sequence 61, Application US/09566921
Patent No. 6682888
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
APPLICANT: Edwards, Carla M.
APPLICANT: BOWARDS: EXPRESSED IN ALZHEIMER'S DISEASE FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM DC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: WOR'D Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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PERL Program
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100.0%; Pre
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FILE REFERENCE: 59.US2.REG
CURRENT FILING DATE: 2000-02-24
CURRENT FILING DATE: 2000-02-24
PRIOR ARPLICATION UNMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 11687
LENGTH: 301
                                                                                                                                                                                                                                                                             RESULT 12
US-09-513-999C-11687/c
US-09-513-999C-11687, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-166-350-32
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                                                                                                                                                                                       APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 61
LENGTH: 3911
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Renal Cancer Associated Antigens and TITLE OF INVENTION: Uses Therefor FILE REFERENCE: L0461/7051
CURRENT APPLICATION NUMBER: US/09/166,350A
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: US 09/166,350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jager, Elke
APPLICANT: Knuth, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6682888 166400.9
TYPE: DNA
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16; Conservative
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100.0%; F1
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100.0%; Pred. No. 11;
1tive 0; Mismatches
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Vedvick, Tom

LICANT: Carter, Darrick

APPLICANT: Retter, Marc

APPLICANT: Mannior, Jane

APPLICANT: Mannior, Jane

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C14

CCURRENT APPLICATION UNMBER: US/09/702,705

CURRENT FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 1833

SOFTWARE: PastSEQ for Windows "
SEQ ID NO 1590

LENGTH: 434

TYPE: DN^*
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US-09-736-457-1590
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                                                                                                   Sequence 1590, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
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                                                                  APPLICANT:
                     APPLICANT:
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NAME/KEY: misc_feature
LOCATION: (1)...(434)
OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc_feature
LOCATION: 274
OTHER INFORMATION: r=a or g
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LOCATION: 244
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                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                             39 GAAACCCTGCTGATG 53
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5. 6504010 .
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Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                                Bangur, Chaitar
Lodes, Michael
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                                                                             Tongtong
r, Chaitanya S.
                                                                                                                                                                                                                                                                                                 23.1%; Score 15; DB 4; Length 434; 100.0%; Pred. No. 39; tive 0; Mismatches 0; Indels
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Sequence 1590, Application US/09614124B

Featent No. 6630574

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Hangur, Chaitanya S.
APPLICANT: Hangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Ratter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: USAGNOSIS OF LUNG CANCER
FULL REFERENCE: 210121.47869
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT ETLING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 434
TYPE: DNA
                                                                                                                                                                                                                                                                                            TYPE: DNA
CRCANISM: Homo sapiens
PERTURE:
NAME/KEY: misc_feature
LOCATION: (1)...(434)
OTHER INFORMATION: n = A,T,C or G
US-09-614-124B-1590
Search completed: December 23, 2004, 01:33:34 Job time: 55.3529 secs
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US-09-614-124B-1590
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TYPE: DNA
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(434)
THER INFORMATION: n = A,T,C or G
US-09-736-457-1590
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FASCSEQ for Windows Version 3.0
SEQ ID NO 1590
LENGTH: 434
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Best Local Similarity
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                                                                                                                                                                                                    Matches
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                                                                                                  20 GARACCCTGCTGATG 34
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                                                                                                                                                                                               23.1%; Score 15; DB 4; Length 434; 100.0%; Pred. No. 39; ative 0; Mismarches 0; Indels
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Word size :
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                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                           Published Applications NA:*

1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*

5: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US08 NEW PUB.seq:*

8: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

10: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

11: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

12: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

14: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

15: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

16: /cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq:*

17: /cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq:*

18: /cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq:*

19: /cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq:*

19: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*

19: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*

20: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
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SUMMARIES
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equence 304, Ap equence 34988, equence 1049, A	De 141376 De 141376 De 141376 De 141376 De 540, AG De 481, I	quence 346, App quence 346, App quence 346, App equence 31722, equence 9856, A	quence 3005; quence 1268; quence 8714; quence 3185; uence 7722, quence 3006; quence 3006; quence 1, Ar quence 2355;	equence 10, equence 112 equence 871 equence 108 equence 871 quence 1374 equence 851 equence 375 equence 112

ALIGNMENTS

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FILTLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of
FILTLE OF INVENTION: Inflammatory and
FILTLE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/09/861,688
CURRENT APPLICATION NUMBER: 08/864,357
PRIOR APPLICATION NUMBER: 08/864,357
PRIOR APPLICATION NUMBER: 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOPTWARE: Patentin version 3.0
SEQ ID NO 6
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Best Local S
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                LENGTH: 65
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                  FEATURE:
61 CGTCC 65
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                                                                                                                        1 GATCCATGGAAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTGCTGATGGACACCC 60
                                                                                     1 GATCCATGGAAATCTGCCCGTCTTTCCAGCGTGTTATCGAAACCCTGCTGATGGACACCC 60
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SEQ ID NO 1
LENGTH: 65
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APPLICANT: Pilon, Aprile L
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhug for the Treatment of
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00260
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Pilon, Aprile L
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REPERENCE: 116142/00170
CURRENT APPLICATION NUMBER: US/09/898,616A
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
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NAME/KEY: misc feature OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
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                                                                                                         OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
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OTHER INFORMATION: Orig
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US-10-647-371-5
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                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment
TITLE OF INVENTION: Inflammatory and
TITLE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/09/861,688
CURRENT FILING DATE: 2001-05-21
CURRENT FILING DATE: 2001-05-21
CURRENT FILING DATE: 2001-05-21
                                                                                                            PRIOR APPLICATION NUMBER: 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
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SEQ ID NO 5
LENGTH: 65
TYPE: DNA
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Publication No. US20040047857A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory
TITLE OF INVENTION: and Fibrotic Conditions
FILE REFERENCE: 116142-85
CURRENT APPLICATION NUMBER: US/10/647,371
CURRENT FILING DATE: 2003-08-25
PRIOR APPLICATION NUMBER: 09/549,926
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 12
FEATURE: OTHER INFORMATION: primer sequence
                                                                          TYPE: DNA
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                                               ORGANISM: Artificial Sequence
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100.0%; Pred. No. 1.3e-27;
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; OTHER INFORMATION: Description of Artificial Sequence: primer sequence US-10-647-371-12
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US-09-861-688-12/c
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TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of
TITLE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/09/861,688
CURRENT FILLNG DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 08/864,357
PRIOR APPLICATION NUMBER: 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
SECTION 012
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SEQ ID NO 12
LENGTH: 42
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Best Local Similarity
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CURRENT FILING DATE: 2003-08-25
PRIOR APPLICATION NUMBER: 09/549,926
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory
TITLE OF INVENTION: and Fibrotic Conditions
FILE REFERENCE: 116142-85
                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                             OTHER INFORMATION: primer sequence
                                                                                                                                                                                                                          FEATURE:
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cal Similarity 100.0%; Pred. No. 3.1e-14;
42; Conservative 0; Mismatches n.
                               43 CCCTGCTGATGGACACCCCGTCC 65
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Application US/10647371
                                                                            Conservative
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100.0%; Pred. No. 0.003
tive 0; Mismatches
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Mismatches 0;
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                                                    ; NAME/KEY: misc_feature
; OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
; OTHER INFORMATION: d sequence maximized for expression in E. coli.
US-09-898-616A-8
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APPLICANT: Claragen Inc.

APPLICANT: Pilon, Aprile L

APPLICANT: Welch, Richard W

TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of

TITLE OF INVENTION: Imflammatory and Fibrotic Conditions

FILE REFERENCE: 116142/00170

CURRENT APPLICATION NUMBER: US/09/898,616A

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: US 08/864,357

PRIOR FILING DATE: 1997-05-28

NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 8
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     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Claragen Inc.
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Alchard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
TITLE OF INVENTION: Imflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00170
CURRENT APPLICATION NUMBER: US/09/898,616A
CURRENT FILING DATE: US/05/898,616A
FRIOR APPLICATION NUMBER: US/08/864,357
PRIOR APPLICATION DATE: 1997-05-28
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 10
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OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
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                                                                                                                                                                        OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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Pred. No.
     Score 23;
  DB 10; Length 60;
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US-10-187-498A-8/c
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US-10-187-498A-7/c
                                                                                                                                                                         Sequence 8, Application US/10187498A
Publication No. US20030207795A1
GENERAL INFORMATION:
APPLICANT: Claragen Inc.
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00260
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT APPLICATION NUMBER: US/01-07-02
PRIOR APPLICATION NUMBER: US/08/864,357
PRIOR APPLICATION NUMBER: US/08/864,357
PRIOR FILING DATE: 2907-05-28
NUMBER OF SEQ ID NOS: 10
SCOTUMARE: PatentIn version 3.1
SEQ ID NO 8
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Publication No. US20030207795A1
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APPLICANT: Welch, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
FILE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00260
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT FILING DATE: 2001-07-02
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PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
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OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
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NAME/KEY: misc_feature
                                               OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
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                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                              TYPE: DNA
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TOTHER INFORMATION: Description of Artificial Sequence: primer sequence
US-10-647-371-11
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                                                                                                                               ; OTHER INFORMATION: primer IRAP5' US-10-129-422-10
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Sequence 11, Application US/10647371; Publication No. US20040047857A1; GENERAL INFORMATION:
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Publication No. US20030166251A1
GENERAL INFORMATION:
APPLICANT: KIM, Sun Young et al.; ViroMed Ltd.
APPLICANT: KIM, Sun Young et al.; ViroMed Ltd.
TITLE OF INVENTION: High efficiency retroviral vector which contain TITLE OF INVENTION: cellular
TITLE OF INVENTION: cellular
TITLE OF INVENTION: non-coding sequence harboring splice acceptor FILE REFERENCE: PCA10935/VML/PCT
                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/129,422
CURRENT FILING DATE: 2002-10-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: KOPATIN 1.5
SEQ ID NO 10
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SEQ ID NO 11
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TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory
TITLE OF INVENTION: and Fibrotic Conditions
FILE REFERENCE: 116142-85
CURRENT APPLICATION NUMBER: US/10/647,371
CURRENT FILING DATE: 2003-08-25
FRIOR APPLICATION NUMBER: 09/549,926
FRIOR APPLICATION NUMBER: 09/549,926
FRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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  1 GATCCATGGAAATCTGC 17
                                               17; Conservative
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ION: High efficiency retroviral vector which contains genetically engir
                                                                  26.2%; Score 17;
100.0%; Pred. No.
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2 GATCCATGGAAATCTGC 18

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US-10-424-599-87144

US-10-424-599-87144, Application US/10424599

Publication No. US2004003107ZA1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-44-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 87144

LENGTH: 647

TYPE: DNA

ORGANISM: Glycine max

FEATURE TERMED TIMESTANCE: --
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Sequence 112555, Application US/10425115

Sequence INFORMATION:

Several INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Chou, Yihua

APPLICANT: Chou, Yihua

APPLICANT: Co, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILNG DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 112555
Search completed: December 23, 2004, 05:19:24 Job time : 920.177~{\rm secs}
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                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_49701C.1 US-10-424-599-87144
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; OTHER INFORMATION: Clone ID: MRT4577_34141C.1
US-10-425-115-112555
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ORGANISM: Zea mays
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AC026895 Homo sapi
AR160920 Sequence
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BC055511 Danio rer
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  Homo sapi
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Homo sapi
   REFERENCE
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AR160921/c
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Unclassified.
1 (bases 1 to 60)
Pilon, A.L., Mukherjee, A.B.
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Pilon, A.L., Mukherjee, A.B. and Zhang, Z.
Use of recombinant human uteroglobin in
and fibrotic conditions
Patent: US 6255281 A 7 03-JUL-2001;
                                                                                                                                                                                                                           Similarity
60; Conserv
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Pred. No. 1.4e-22;
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Allen, N.,

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37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-MAR-2002) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:yn@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Stropphyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T., Sato,S. and Tabata,S. Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Sixty-six TAC clones which cover the 6.7 M. Regions of the Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG
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AP004967.1 GI:21907985
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                                                                                                                                                                                                                                                                                                       l Similarity
19; Conserv
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  Homo sapiens chromosome 2 clone RP11-396J2
SEQUENCE, 22 unordered pieces.
AC026895
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                                                                                                                                                                                                        AAGCAGCTATGGAACTGTT 87184
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/mol_type="genomic DNA"
/variety="Japonicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="LjT27L02"
/clone_lib="LjT library"
/note="TAC clone:TM0144~synonym: Lotus japonicus"
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'chromosome="1"
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Pred. No.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 2, clone RP11-396J2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-MAR 2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 19, 2000 this sequence version replaced gi:7328755.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Center clone name: 396 J 2

Center clone name: 396 J 2

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 184437 bases at least Q40
Consensus quality: 194805 bases at least Q30
Consensus quality: 197132 bases at least Q20
Insert size: 120040; agarose-fp
Insert size: 198749; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence submissions@genome.wi.mit.edu
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             7: contig of 1067 bp i
7: gap of 100 bp
5: contig of 1689 bp i.
5: gap of 100 bp
1: contig of 3027 bp ii
5: gap of 100 bp
                  100 bp
of 3027 bp in length
100 bp
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7884 10616 10716 12693

gap of 100 bp contig of 1977 bp in length gap of 100 bp contig of 2167 bp in length

contig of 1700 bp in length gap of 100 bp contig of 2732 bp in length

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ACCESSION
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                                                                                                                                                                                    59 AGGACATGCGTGAAGCAG 42
                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 59)
Pilon,A.L., Mukherjee,A.B. and Zhang,Z.
Use of recombinant human uteroglobin in treatment of inflammatory and fibrotic conditions
Patent: US 6255281-A 11 03-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 bp
Sequence 11 from patent US 6255281.
AR160920
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            Homo sapiens (human)
Homo sapiens
                                                                      BV203590 PA STS 10-JUN-200-
sqnm212590 Human DNA (Sequenom) Homo Bapiens STS genomic, sequence
tagged site.
BV203590
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                        BV203590.1 GI:48173010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown.
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88151. .98020
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/note="assembly_fragment
                                                                                                                                                                                                                                                                                                           /organism="unknown"
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165334. .200849
/note="assembly_fragment"
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108381. .126228
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126329. .165233
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66357. .77020
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tive 0; Mismatches
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108281 108381 126229

108380: Gentig of 10160 bp in length 108380: gap of 100 bp 126228: contig of 17848 bp in length 126328: gap of 100 bp 165333: contig of 38905 bp in length 165333: gap of 100 bp 200849: contig of 35516 bp in length.

66357 77021 77121 88051 88151 98021 98121

gap of 100 bp contig of 9870 bp in length gap of 100 bp

46514 55510

gap of

tig of 6973 bp in length of 100 bp tig of 8896 bp in length of 100 bp

gap of 100 bp contig of 10647 bp in length gap of 100 bp

contig of 10664 bp in length gap of 100 bp contig of 10930 bp in length

39441

gap of 100 by contig of 7906 bp in length gap of 100 bp in length

gap of 100 bp contig of 2802 bp in length gap of 100 bp in length

gap of 100 bp contig of 4705 bp in length

gap of 100 bp contig of 4366 bp in length

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of 100 bp g of 4202 bp in length

source

/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="2"

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10716. .12692

/note="assembly_fragment"

note="assembly_fragment" 'note="assembly_fragment"

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(bases i to 201)

Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
                                                                                                                                                         STS size: 201
                                                                                                                                                                          Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
                                                                                                                                                                                                                                                       3595 John Hopkins Court, San Diego,
Tel: 18582029018
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1 (bases 1 to 201)

Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal; C.R., Shi,M.M., Cantor,C.R. and Braun,A.

Carge-Scale Validation of Single Nucleotide Polymorphisms in Gene
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Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 201.
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Tel: 18582029018
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/db_xref="taxon:9606"
/clone lib="Human DNA (Sequenom)"
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/mol type="genomic DNA"
/db xref="taxon:9606"
/clone_lib="Human DNA (Sequenom)"
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Sequence 1284 from Patent WO0212328
AX397069
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1 (bases 1 to 201)

Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.

Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Patent: WO 0212328-A 1284 14-FEB-2002;
                                  King, G.E., Meagher, M.J., \text{Xu,J.} and Secrist, H. Compositions and methods for the therapy and diagnosis of colon
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                        Homo sapiens
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3595 John Hopkins Court, San Diego, CA 92121, USA
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BV203592
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Fax: 18582029020
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tive 0; Mismatch
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        1428 bp
Human SF2p33 mRNA, complete cds.
M69040 GI:338046
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OS Homo sapiens (human)
PN WO 0125427-A/31
PD 12-APR-2001
PF 02-OCT-2000 WO 2000JP006840
PR 01-OCT-190 JP 99P 280976
PI HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, PI AYAKO KAWABATA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1428)

Nojima, H., Yoshisue, H., Obayashi, M., Ota, T., Kawabata, A., Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S. Shear stress-responsive DNAs; Patent: WO 0125427-A 31 12-APR-2001; KYOWA HAKKO KOGYO CO LTD, HIROSHI NOJIWA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, AYAKO KAWABATA, KAZUHIRO SAKURADA, TETSURO KUGA SUSUMU SEKINE, YUSUKE NAKAMURA, SUMIO SUGANO OS HOMO Sapiens (human)

PN WO 0125427-A/31

PN WO 0125427-A/31
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WO 0125427-A/31.
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                                                                                                                                                                                                                                                                                                                                                  A61K48/00,A61P9/10,G01N33/50,G01N33/53
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                                                                                                                                                                                                                                                                                                                                                                            C12N15/12, C07K14/435, C07K16/18, C12P21/02, C12Q1/68, A61K38/00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORPORATION (US)
                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                     30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.0%;
                                                                                                                                                                     %; Score 18; DB |
%; Pred. No. 34;
0; Mismatches
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                          125). . (868)
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DNAs
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                                                                                                                                                                                     DB 6;
34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
38;
                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                Length 1428;
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                                                 linear
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                                               PRI 24-NOV-1993
                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KUGA,
                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                            3'UTR
ORIGIN
                                                                                                            BC042354
LOCUS
DEFINITION
                                                        ACCESSION
VERSION
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                                              KEYWORDS
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AUTHORS
TITLE
                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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                  ORGANISM
                                                                                                                                                                                                                                                               Query Match
Best Local
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MEDLINE
PUBMED
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5'UTR
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                                                                                                                                                                                                                        41
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                   18;
                                                          BC042354.1
                                                                                                                                                                                                                                                               Similarity
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Original source text: Homo sapiens cDNA to mRNA.

Comments: SF2p33 is an essential pre-mRNA splicing factor, which can also affect alternative 5' splice site selection in vitro by stimulating the use of proximal 5' splice sites.

(Krainer, A.R., Conway, G.C., and Kozak, D. (1990) Purification and Characterization of SF2, a Human Pre-mRNA Splicing Factor: Genes Dev. 4, 1158-1171; Krainer, A.R., Conway, G.C., and Kozak, D. (1990) The Essential Pre-mRNA Splicing Factor SF2 Influences 5' Splice Site Selection by Activating Proximal Sites. Cell 62, 35-42). This factor is also known as ASF (Ge, H., and Manley, J.L. (1990) A protein Factor, ASF, Controls Alternative Splicing of SV40 Barly Pre-mRNA In Vitro. Cell 62, 25-34). SF2 p33 consists of two polypeptides of apparent molecular weight 33 kd, approximately, although their predicted molecular weight 527,744 daltons. The two forms appear to differ by the extent of post-translational modification, which includes phosphorylation. SF2p33 binds RNA and promotes the annealing of complementary RNAs. It is required for assembly of pre-spliceosome complexes. The Location/Qualifiers

1 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                 543 ACATGCGTGAAGCAGGTG 560
                                                                                                                                       Xenopus laevis similar to splicing factor, arginine/serine-rich; (splicing factor 2, alternate splicing factor), mRNA (cDNA clone INAGE:4681465), partial cds.
Xenopus laevis (African clawed Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1428).

Krainer, A.R., Mayeda, A., Kozak, D. and Binns, G.

Functional expression of cloned human splicing factor SF2: homology to RNA-binding proteins, UI 70K, and Drosophila splicing regulators Cell 66 (2), 383-394 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATGCGTGAAGCAGGTG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="SF2p33"
/protein_id="AAA03476.1"
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/db_xref="G1:338047"
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GGGGAPRGRYGPPSRRSENRVVVSGLPPSGSWQDLKDHMREAGDVCYADVYRDGTGVV
EFVRKEDMTYAVRKLDNTKFESHEGETAYINVKVDGPRSPSYGRSRSRSRSRSRSRSRSRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNSRSRSYSPRRSRGSPRYSPRHSRSRSRT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function="pre-mRNA splicing factor"
                                                                                                   GI:27503246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1428;
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PUBMED
REFERENCE
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TITLE
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Klausmer, R.D., Collins, F.S., Wagner, L., Schemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheefer, C.F., Bhat, N.K.,
Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (02-VAN-2003) National Institutes of Health, Xenopus Gene
Collection (XGC), National Institute of Child Health and Human
Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   passed the following identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Flate: 94 Row: b Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. (LLNL) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org http://www.systemsbiology.org http://www.system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project
Contact: XGC help desk
Email: ogapbs=r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev. Dyn. 225 (4), 384-391 (2002)
12454917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 1618)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          initiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
/gene="Sfrs1"
/codon_start=2
                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:4681465"
/tissue type="Embryo, stage 31/32, Xenopus"
/clone lib="NICHD_XGC_Emb4"
/lab_host≈"pH108"
                                                                                                                                                                                                                                                                           note="Vector: pCMV-SPORT6"
                                                                                                                                          db_xref="LocusID:399226"
                                                                                                                                                                                            gene="Sfrsl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism≃"Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type="mRNA"
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HUMASF
LOCUS
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ACCESSION
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          525 ACATGCGTGAAGCAGGTG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 ACATGCGTGAAGCAGGTG 58
                                                                                                                                                                                                                                                        Original source text: Homo sapiens cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                              Ge,H., Zuo,P. and Manley,J.L.
Primary structure of the human splicing factor ASF reveals similarities with Drosophila regulators
Cell 66 (2), 373-382 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alternative splicing factor. Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1717)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M72709
M72709.1 GI:179073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human alternative splicing factor mRNA, complete cds
                                                                                                                                                                                                                                                                                          1855257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /notes=RRM 1; Region: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain). The RRM motif is probably diagnostic of an RNA binding protein. RRMs are found in a variety of RNA binding proteins, including various hnRNP proteins, proteins implicated in regulation of alternative splicing, and protein components of anRNPs The motif also appears in a few single stranded DNA binding proteins. The RRM structure consists of four strands and two helices arranged in an alpha/beta sandwich, with a third helix present during RNA binding in some cases The C-terminal beta strand (4th strand) and final helix are hard to align and have been omitted in the SEED alignment The LA proteins have a N terminus rrm which is included in the seed. There is a second region towards the C terminus that has some features of a rrm but does not appear to have the important structural core of a rrm. The LA proteins are of the main autoantigens in Systemic lupus erythematosus (SLE), an autoimmune disease"
/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/cell line="HeLa"
join(I. .648,831..1717)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Sfr81 protein"
/protein_id="AAH42354.1"
/protein_id="AAH42354.1"
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LEVERTAKIRVKVDGPRSPSYGRSRSRSRSRSRSRSRSRSNSRSRSYSPRRSRGSPRYSPRH
EGETAKIRVKVDGPRSPSYGRSRSRSRSRSRSRSRSRSNSRSRSYSPRRSRGSPRYSPRH
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476. .658
                                                                                                                                                                                          Cocation/Qualifiers
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100.0%; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region: RNA recognition motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1717 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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ACCESSION
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BC056752
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Strausberg,R.I., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Pubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 ACATGCGTGAAGCAGGTG 58
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                   Danio rerio cDNA clone MGC:65898 IMAGE:6801570,
BC056752
                                                                                                                                                                                                                               Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                     BC056752.1
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848. .1717
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/label=1b
831. .171
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649. .830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSGGGVIRGPAGNNDCRIYVGNLPPDIRTKDIEDVFYKYGAIRD IDLKNERGGPPFAFVEFEDPRDAEDAVVGRDGYDYDGYDYDYDFFRSGGGGGGGGGAPRGFYGPAFVEFEDFRDAEDAVVGRDGYYLRVEFPRSGGGGGGGGGGAPRGRYGOPPSRESERVVVSGLPPSGSWDDLKDHWEBAGDVCYADVYRDGTGVVEFYKEDMTYAVRKLDNTKFRSHEFCLSNREKLPTSGLKLMGFEVQVMEDLDLEAVVVAEAVRAEATAGVAVTPGGEAEDHHAILFVIADLALVHXMIGDTFCRTHVVYSFFLFSTIFSENCFVSOKCFVONGLKC"
FSFFNSNCFVONGLKC"
join(97...648,848...1042)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAA35565.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA35564.1"
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                                                                                                                                                                                                                                                                                     GI:34785173
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                    complete
                                                                                                                                                                                                        Euteleostomi;
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8

41 ACATGCGTGAAGCAGGTG

58

Matches Query Match

18;

Conservative

30.0%; Score 18; 100.0%; Pred. No. tive 0; Mismatc

Mismatches 33; ູ ຫ

Length 1860,

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Similarity

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TITLE
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McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Bickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LINI at: http://image.llnl. Series: IRAK Plate: 121 Row: p Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency Operator of the following selection criteria: Hexamer frequency operators: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.misc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Bietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (25-AUG-2003) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Chi-Bin Chien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                          note="Vector:
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                                                                                                                                                                                                                                                                                                                      pCMV-SPORT6.1"
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611 ACATGCGTGAAGCAGGTG 628

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BC055511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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Klausner, R.D., Collins, F.S., Wagner, L., Schemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schefer, C.F., Bhat, N.K.,
Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skaiska, J., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Mazra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Sumio Sugano
CDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IPAK Plate: 122 Row: f Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cyprinidomes, Cyprinidae, Danio.

1 (bases 1 to 2002)
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Search completed: December 22, 2004, 23:36:31
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Minimum DB seg length: 0
Maximum DB seg length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21	20	19	18	17	16	15	14	13	12	11	10	9		c 7	0 6	a v	Ω 4	α 3	2	ш	Result
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28.3	30.0	30.0		30.0		0	30.0	30.0	30.0	30.0	30.0	30.0	0	30.0	61.7	61.7	61.7	61.7	100.0	100.0	Query
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AAS18797	ADK70081	ADK70082	ADI22703	ADQ22406	ADI15992	ADD22452	ADP07658	ADH28741	AAL60055	AAH02904	ACH35932	ABK45733	ADL27631	ABZ58375	ADL27632	ADL27633	ABZ58377	ABZ58376	ADL27627	ABZ58371	ID
Aas18797 PCR prime	Adk70081 Wild type	Adk70082 Mutant hu	Adi22703 Human liv	Adq22406 Human sof	Adi15992 Human PP	Add22452 HLA-B46 T	Adp07658 Human sec	Adh28741 Human chr	Aal60055 Human Pc0	Aah02904 Human she	Ach35932 Human end	Abk45733 cDNA enco	Adl27631 Recombina	Abz58375 Human ute	Adl27632 Recombina	Adl27633 Recombina	Abz58377 Human ute	Abz58376 Human ute	Adl27627 Recombina	Abz58371 Human ute	Description

4.5	44	43	42	41	C 40		38	c 37	36	c 35		. 33			c 30		28	27	26	25	c 24	23	22
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26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	28.3
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ADD47860	ADD47032	ADC38821	AAX76396	ACF12861	AAK81667	ABD09565	ABD09379	ADM03518	ADD18824	ACF64695	AAS59766	ABK13152	AAC49282	ADI31178	AAZ16289	AAZ17762	ADA30641	ABX50810	ADL85789	ADL85790	AAZ14356	ABN56135	ABN59992
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Add47860	Add47032	Adc38821	Aax76396	Acf12861	Aak81667	Abd09565	Abd09379	Adm03518	Add18824	Acf64695	Aas59766	Abk13152	Aac49282	Adi31178 Human cDN	Aaz16289 Human gen	Aaz17762	Ada30641	Abx50810	Ad185789	Ad185790	Aaz14356	Abn56135	Abn59992

ALIGNMENTS

ABZ58371;

ABZ58371 standard; DNA; 60

BP.

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RESULT 1
ABZ59371
ID 28-A
XX ABZ5
XX ABZ5
XX ABZ5
XX ABZ5
XX Homa
DH Huma
XX Homa
COS Synt
XX ADZ5
XX ADZ5
XX ADZ5
XX Homa
COS Synt
XX ADZ5
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pilon AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001; 2001US-00898616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2002; 2002WO-US020836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human uteroglobin synthetic gene oligonucleotide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-2003
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Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic gene which codes for human uteroglobin.

WPI; 2003-221527/21.

Claim 1; Page 33; 127pp; English.

The present sequence is that of oligonucleotide 2, which was used in the construction of a synthetic gene for the production of human uteroglobin (hUG) in bacteria. Oligonucleotides 1-4 (see ABZ58370-73) were used to assemble the coding strand and oligonucleotides 5-8 (see ABZ58374-77) the complementary strand. The gene was assembled by annealing and ligation of the oligonucleotides. Because mature native hUG has glutamic acid at its N-terminus, an initiator methionine was added to the N-terminus, and

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RESULT 2
ADL27627
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Matches 60
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of recombinant human uteroglobin (rhUG), comprising a synthetic gene or human cDNA sequence which codes for human UG, constructed from the oligonucleotides appearing as ADL27626-ADL27629, and which further comprises Met-Ala-Ala at the N-terminus of the sequence. Also included are producing an rhUG master cell bank (comprising inoculating a suitable incubating broth with an aliquot portion of a rhUG research seed bank to form a bacterial culture, incubating the bacterial culture, adding a cryopreservative to the bacterial culture to form a cryopreserved solution, transferring a portion of the cryopreserved solution to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; recombinant human uteroglobin; rhUG; bacterial expression system; rhUG master cell bank; bacterial expression system; rhUG master cell bank; rhUG research seed bank; anti-inflammatory; secretory phospholipase A fibronectin; respiratory distress; inflammation; fibrotic disease.
                                                                                                                                                                                                                                                                                     Bacterial expression system for production of recombinant human uteroglobin comprising synthetic gene or human cDNA sequence which codes
                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-051527/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-1997; 97US-00864357
02-JUL-2001; 2001US-00898616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant human uteroglobin,
                                                                                                                                                                                                                             Claim 1; SEQ ID NO 2; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           Pilon AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2002; 2002US-00187498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acute renal failure, rheumatoid arthritis and asthma
                                                                                                                                                                                      The invention relates to a bacterial expression system for the production
                                                                                                                                                                                                                                                                        for human uteroglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PILO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                    (WELC/) WELCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACCAGGACCATGCGTGAAGCAGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 BP; 15 A; 15 C; 18 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACCAGGACATGCGTGAAGCAGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                           Welch RW
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rhUG, coding oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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cc cryovial and storing the oryovial at a temperature below -60 degrees C), c expressing rhUG (comprising providing a production seed cell bank culture comprising an expression vector capable of expressing rhUG, inoculating a broth medium with the production seed cell bank culture to form an controlled in incubating the bacterial culture formed in step (b), inoculating a large scale fermenter with the inoculum formed from the step (c) to form a fermentation culture, incubating the fermentation culture within the large scale fermenter, adding an induction agent to culture within the large scale fermenter, adding an induction agent to the fermentation culture, induce the expression of rhUG and harvesting the above fermentation culture, purifying rhUG, determining the potency of rhUG in a sample, measuring in vitro anti-inflammatory effect arising crom inhibition or blocking of secretory phospholipses A 2 enzymes by cr rhUG, measuring in vitro binding of rhUG to fibronectin, determining the purity of rhUG, and a pharmaceutical composition comprising a purified cr producing a rhUG research seed bank or a pharmaceutial grade rhUG distress. The present sequence is a coding strand oligonucleotide used to control to the present sequence is a coding strand oligonucleotide used to
                                                          construct the synthetic rhUG gene.
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                                                                              Query Match
                                                                                                           Sequence 60 BP; 15 A; 15 C; 18 G; 12 T; 0 U; 0 Other;
                                                                    госат
 -
                                                                  Similarity
                   AGCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACCAGGACATGCGTGAAGCAGGTGCT
 AGCTACGAAGCAGCTATGGAACTGTTCTCCCGGACCAGGACATGCGTGAAGCAGGTGCT 60
                                                      Conservative
                                                                 100.0%;
                                                      0
                                                                  Score 60; DB 12;
Pred. No. 5.2e-23;
                                                      Mismatches
                                                                                 Length
                                                        Indels
                                                      0
                                                     Gaps
                            60
                                                        0
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RESULT 3
ABZ58376/c
ID ABZ583
XX 28-APR
DT 28-APR
XX 28-APR
XX Human;
XX Human;
XX antiin
XX antiar
XX antiar
XX antiar
XX antiar
XX CliAR-
XX 02-UUL
XX 02-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; uteroglobin; respiratory distress; antiinflammatory; antifibrotic; antiinflammatory; antiasthmatic; nephrotropic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human uteroglobin synthetic gene oligonucleotide 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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02-JUL-2001; 2001US-00898616. WPI; 2003-221527/21. Pilon AL, (CLAR-) CLARAGEN INC 02-JUL-2002; 2002WO-US020836 Welch RE;

Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic gene which codes for human uteroglobin.

Example 1; Page 33; 127pp; English

The present sequence is that of oligonucleotide 7, which was used in the construction of a synthetic gene for the production of human uteroglobin (hUg) in bacteria. Oligonucleotides 1-4 (see ABZ58370-73) were used to assemble the coding strand and oligonucleotides 5-8 (see ABZ58374-77) the

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RESULT 4
ABZ583
XX
ABZ583
AC
ABZ583
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Best Local :
The present sequence is that of oligonucleotide 9, which was used in the construction of a synthetic gene for the production of human uteroglobin (hUG) in bacteria. Oligonucleotides 1-4 (see ABZ58370-73) were used to assemble the coding strand and oligonucleotides 5-8 (see ABZ58374-77) the complementary strand. The gene was assembled by annealing and ligation of the oligonucleotides. Because mature native hUG has glutamic acid at its v-terminus, an initiator methionine was added to the N-terminus, and codon usage was optimised for expression in bacteria. In an example from the invention, the synthetic gene was cloned into plasmid pCG12 (see ABZ58378) and recombinant hUG (see ABP72259) was produced in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementary strand. The gene was assembled by annealing and ligation of the oligonucleotides. Because mature native MUG has glutamic acid at its N-terminus, an initiator methionine was added to the N-terminus, and codon usage was optimised for expression in bacteria. In an example from the invention, the synthetic gene was cloned into plasmid pCG12 (see ABZ58378) and recombinant hUG (see ABZ58378) was produced in Escherichia coli strain CG12. The invention relates generally to the production of recombinant hUG by bacterial expression, protein purification and scaled-recombinant hUG is useful for the treatment of inflammatory and fibrotic conditions, such as neonatal respiratory distress syndrome and bronchopulmonary dysplasia. It may also be used to treat conditions associated with elevated phospholipase A2 levels such as pancreatitis, accute renal failure, rheumatoid arthritis and asthma
                                                                                                                                                                                                                                                                                                                                           Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic
                                                                                                                                                                                                                                                                            Example 1; Page 33; 127pp; English.
                                                                                                                                                                                                                                                                                                                              gene which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-2001; 2001US-00898616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; antiasthmatic; nephrotropic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; uteroglobin; respiratory distress; antiinflammatory; antifibrotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human uteroglobin synthetic gene oligonucleotide 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABZ58377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60 BP; 12 A; 14 C; 22 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CLAR-) CLARAGEN INC
                                                                                                                                                                                                                                                                                                      treating inflammatory .... --
e which codes for human uteroglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                             2003-221527/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGCTACGAAGCAGCTATGGAACTGTTCTCCCGGACC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Welch RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
2.1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 5
ADL27633/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                           Bacterial expression system for production of recombinant human uteroglobin comprising synthetic gene or human cDNA sequence which codes for human uteroglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli strain CG12. The invention relates generally to the production of recombinant hUG by bacterial expression, protein purification and scaled-up production according to current good manufacturing practices. The recombinant hUG is useful for the treatment of inflammatory and fibrotic conditions, such as neonatal respiratory distress syndrome and bronchopulmonary dysplasia. It may also be used to treat conditions associated with elevated phospholipase A2 levels such as pancreatitis, accute renal failure, rheumatoid arthritis and asthma
                                                                                                                                                                                                                                                                                          Pilon AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL27633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 60 BP; 12 A; 14 C; 22 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                WPI; 2004-051527/05
                                                                                                                                                                                                                                                                                                                                                          28-MAY-1997;
02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003207795-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ss; recombinant human uteroglobin; rhUG; bacterial expression system; rhUG master cell k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant human uteroglobin, rhUG, non-coding oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL27633 standard; DNA; 60
                                                                                                                                                                                                                                                                                                                   (PILO/) PILON A L. (WELC/) WELCH R W.
                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2002; 2002US-00187498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibronectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterial expression syst
rhUG research seed bank;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACC 37
                                                                                                                                                                                                                                                                                          Welch RW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                           2001US-00898616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h seed bank; anti-inflammatory; secretory phospholipase A
respiratory distress; inflammation; fibrotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                         97US-00864357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 9; Pred. No. 2.1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bank;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scaled-
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The invention relates to a bacterial expression system for the production of recombinant human uteroglobin (rhUg), comprising a synthetic gene or human cDNA sequence which codes for human UG, constructed from the oligonucleotides appearing as ADL27626-ADL27629, and which further comprises Met-Ala-Ala at the N-terminus of the sequence. Also included are producing an rhUG master cell bank (comprising inoculating a suitable incubating broth with an aliquot portion of a rhUG research seed bank to form a bacterial culture, incubating the bacterial culture to form a cryopreserved solution, transferring a portion of the cryopreserved solution to a cryovial and storing the cryovial at a temperature below -60 degrees C), expressing rhUG (comprising providing a production seed cell bank culture accomprising an expression vector capable of expressing rhUG, inoculating a

Example 1; SEQ ID NO 8; 64pp; English.

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RESULT 6
ADL27632/c
ID ADL27632 standard; DNA;
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc broth medium with the production seed cell bank culture to form an cc inocultum, incubating the bacterial culture formed in step (b), and a large scale fermenter with the inocultum formed from the cc inoculating a large scale fermenter with the incubating the fermentation culture, incubating the fermentation culture, incubating the fermentation culture to induce the expression of rhUG and harvesting the above fermentation culture), purifying rhUG, determining the potency cc frug in a sample, measuring in vitro anti-inflammatory effect arising cc rhUG, measuring in vitro binding of rhUG to fibronectin, determining the purity of rhUG, and a pharmaceutical composition comprising a purified cc rhUG, measuring in vitro binding of rhUG to fibronectin, determining the purity of rhUG, and a pharmaceutical composition comprising a purified cc rhUG and a carrier or diluent. The bacterial expression system is useful cc distress. The present sequence is a non-coding strand oligonucleotide considered the content of the present sequence is a non-coding strand oligonucleotide considered the content of the present sequence is a non-coding strand oligonucleotide considered the content of the content of the present sequence is a non-coding strand oligonucleotide considered the content of the coding substance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                     Bacterial expression system for production of recombinant human uteroglobin comprising synthetic gene or human cDNA sequence which codes
                                                                                                                                                                                                                                                                                                                                                          28-MAY-1997; 97US-00864357
02-JUL-2001; 2001US-00898616
                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2002; 2002US-00187498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003207795-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; recombinant human uteroglobin; rhUG; bacterial expression system; rhUG master cell bank; rhUG research seed bank; anti-inflammatory; secretory phospholipase A 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAY-2004 (first entry)
                                                                                                                                                                                                                    WPI; 2004-051527/05.
                                                                                                                                                                                                                                                             Pilon AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibronectin; respiratory distress; inflammation; fibrotic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant human uteroglobin, rhUG, non-coding oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 60 BP; 12 A; 14 C; 22 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used to construct the synthetic rhUG gene.
                                                                                                                                  for human uteroglobin.
                                                                                                                                                                                                                                                                                                                     (PILO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACC 37
                                                                                                                                                                                                                                                                                                  PILON A L. WELCH R W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTÁCGAAGCAGCTÁTGGAACTGTTCTCTCCGGÁCC 1
                                                                                                                                                                                                                                                             Welch RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                97US-00864357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 12;
; Pred. No. 2.1e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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of recombinant human uteroglobin (rhVG), comprising a synthetic general numan cDNA sequence which codes for human UG, constructed from the coligonucleotides appearing as ADL27626-ADL27629, and which further

The invention relates to a bacterial expression system for the production

gene or

Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic gene which codes for human uteroglobin.

Example 1; SEQ ID NO 7; 64pp; English.

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RESULT 7
ABZ5835/c
ID ABZ583
XX ABZ583
XX 28-APR
DT 28-APR
XX Human;
KW Human;
KW antian
KW antian
XX WO2003
XX 02-JUL
XX 02-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            666666666666666666666666666666688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC comprises Met-Ala-Ala at the N-terminus of the sequence. Also included are producing an rhUG master cell bank (comprising inoculating a suitable includating broth with an aliquot portion of a rhUG research seed bank to CC form a bacterial culture, incubating the bacterial culture, adding a CC cryopreservative to the bacterial culture to form a cryopreserved a CC cryopreservative to the bacterial culture to form a cryopreserved a CC cryopreserved in and storing the cryovial at a temperature below -60 degrees C), CC expressing rhUG (comprising aportion of the cryopreserved solution to a ccyopresial and storing the production seed cell bank culture comprising an expression vector capable of expressing rhUG, inoculating a broth medium with the production seed cell bank culture to form an CC inoculating a large scale fermenter with the inoculaure form and form a fermentation culture, incubating the fermentation culture to form an CC culture within the large scale fermenter, adding an induction agent to the fermentation culture to induce the expression of rhUG and harvesting the above fermentation culture), purifying rhUG, determining the potency cof rhUG, measuring in vitro binding of rhUG and carrier or diluent. The bacterial expression system is useful CC purity of rhUG, and a pharmaceutical composition comprising a purified cryoducing a rhUG is safe to administer to a patient in respiratory diseases. The present sequence is a non-coding strand oligonuclectide construct the synthetic rhUG gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                        WPI; 2003-221527/21.
                                                                                                                                                                                                                                      Pilon AL,
                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001US-00898616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003003979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synchetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; uteroglobin; respiratory distress; antiinflammatory; antifibrotic; antiinflammatory; antiasthmatic; nephrotropic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human uteroglobin synthetic gene oligonucleotide 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ58375 standard; DNA; 59 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 60 BP; 12 A; 14 C; 22 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2002; 2002WO-US020836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarthritic; ss.
                                                                                                                                                                                                                                                                                                           (CLAR-) CLARAGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 AGCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                      Welch RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 8
ADL27631/c
ID ADL276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of oligonucleotide 6, which was used in the construction of a synthetic gene for the production of human uteroglobin in bacteria. Oligonucleotides 1.4 (see ABZ58370-73) were used to assemble the coding strand and oligonucleotides 5-8 (see ABZ58374-77) the complementary strand. The gene was assembled by annealing and ligation of the oligonucleotides. Because mature native hUG has glutamic acid at its N-terminus, an initiator methionine was added to the N-terminus, and codon usage was optimised for expression in bacteria. In an example from the invention, the synthetic gene was cloned into plasmid poc[2] (see ABZ58378) and recombinant hUG (see ABP72259) was produced in Escherichia coli strain CG12. The invention relates generally to the production of recombinant hUG by bacterial expression, protein purification and scaled-cup productions according to current good manufacturing practices. The recombinant hUG is useful for the treatment of inflammatory and fibrotic conditions, such as neonatal respiratory distress syndrome and scaled-bronchopulmonary dysplasia. It may also be used to treat conditions associated with elevated phospholipase A2 levels such as pancreatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                    28-MAY-1997; 97US-00864357.
02-JUL-2001; 2001US-00898616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; recombinant human uteroglobin; rhUG; bacterial expression system; rhUG master cell bank; rhUG research seed bank; anti-inflammatory; secretory phospholipase A fibronectin; respiratory distress; inflammation; fibrotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 59 BP; 9 A; 17 C; 15 G; 18 T; 0 U; 0 Other;
                                                                      uteroglobin comprising synthetic gene or for human uteroglobin.
                                                                                                               Bacterial expression system for production of recombinant human
                                                                                                                                                      WPI; 2004-051527/05.
                                                                                                                                                                                         Pilon AL,
                                                                                                                                                                                                                                                                                                                                             02-JUL-2002; 2002US-00187498
                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                        US2003207795-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant human uteroglobin, rhUG, non-coding cligonucleotide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL27631 standard; DNA; 59 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acute renal failure, rheumatoid arthritis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 33; 127pp; English.
                                                                                                                                                                                                                              (PILO/) PILON A L. (WELC/) WELCH R W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 AGGACATGCGTGAAGCAG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 AGGACATGCGTGAAGCAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                         Welch RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.0%; Score 18; DB 9; Length 59; 100.0%; Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                            human cDNA sequence which codes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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The invention relates to a bacterial expression system for the production

New colon cancer polypeptides and polynucleotides, useful as vaccines

Example 1; SEQ ID NO 6; 64pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC chuman cDNA sequence which codes for human UG. comprising a synthetic gene or coligonuclectides appearing as ADL27629, and which further CC comprises Met-Ala-Ala at the N-terminus of the sequence. Also included CC are producing an rhUG master cell bank (comprising inoculating a suitable CC incubating both with an aliquot portion of a rhUG research seed bank to CC form a bacterial culture, incubating the bacterial culture, adding a CC cryopreservative to the bacterial culture to form a cryopreserved CC solution, transferring a portion of the cryopreserved cell bank (comprising an expression vector capable of expressing rhUG. inoculating a continue comprising an expression vector capable of expressing rhUG. inoculating a both medium with the production seed cell bank culture coinculating a large scale fermenter with the inoculum formed from the bacterial culture formed in step (b), containing a large scale fermenter, adding an induction agent to culture within the large scale fermenter, adding an induction agent to continue within the large scale fermenter, adding an induction agent to continue formed from the sample, measuring in vitro anti-inflammatory effect arising coff from inhibition or blocking of secretory phospholipase A 2 enzymes by ridig, measuring in vitro anti-inflammatory effect arising the for producing a rhUG research seed bank or a pharmaceutical grade rhUG construct the supersult or a patient in respiratory colisters. The present sequence is a non-ocding strand oligonucleotide cused to construct the synthetic rhUG gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                    03-AUG-2000; 2000US-0223283P.
28-MAR-2001; 2001US-0279763P.
29-JUN-2001; 2001US-0302051P.
                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                             gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding colon tumour protein, SEQ ID No 1284.
                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK45733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK45733 standard; cDNA; 432 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 59 BP; 9 A; 17 C; 15 G; 18 T; 0 U; 0 Other;
                                  WPI; 2002-241739/29.
                                                                  King GE,
                                                                                                                                                                                                        31-JUL-2001; 2001WO-US024218.
                                                                                                                                                                                                                                                                           W0200212328-A2.
                                                                                                                                                                                                                                                                                                                                                             Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
                                                                                                                                                                                                                                         14-FEB-2002.
                                                                                                     (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to construct the synthetic rhUG gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 AGGACATGCGTGAAGCAG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGACATGCGTGAAGCAG 42
                                                                  Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.0%; Pr/
100.0%; Pr/
0;
                                                                     Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18;
Pred. No.
                                                                     Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 59 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 10
ACH35932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 18
The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also
                                                                                                                      New polynucleotide sequences obtained from various cDNA libraries, as hybridization probes, as oligomers for PCR, for chromosome and guapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human endothelial cell cDNA #4065.
                                                                   Claim 1; SEQ ID NO 23144; 44pp; English.
                                                                                                         antisense DNA or RNA.
                                                                                                                                                                                             WPI; 2003-615964/58.
                                                                                                                                                                                                                           Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                  30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                                                                                                                                                                                       17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACH35932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 432 BP; 123 A; 85 C; 103 G; 121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer. ABK4450-ABK46237 represent coding sequences of human colon tumour proteins of the invention. Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as
                                                                                                                                                                                                                                                                                 (STAC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACH35932 standard; cDNA; 489 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1284; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                 (JONE/)
                                                                                                                                                                                                                                                                                                                                  (DRMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 ACATGCGTGAAGCAGGTG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
                                                                                                                                                                                                                                                           JONES L W.
                                                                                                                                                                                                                                                                                                                              DRMANAC R T.
                                                                                                                                                                                                                                                                                               STACHE-CRAIN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATGCGTGAAGCAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.0%; Score 18; DB 6; 100.0%; Pred. No. 5.6;
                                                                                                                                                                                                                             Stache-Crain B, Dickson MC,
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                                                                                                                                                                                                                             Jones LW;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polypucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated DNA/EST sequences. Note: The sequence data obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID-20030073623
Sequence 1428 BP; 341 A; 296 C; 400 G; 391 T; 0 U; 0 Other;
                                               The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in t diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                 Claim 20; Page 386-388; 678pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human shear stress-response coding sequence SEQ ID NO: 61.
                                  hypertension
                                                                                                                                                                                DNA sequences, proteins encoded by them and antibodies against useful in diagnosis and treatment of vascular disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                      arterioscierosis.
                                                                                                                                                                                                                                    WPI; 2001-266308/27.
P-PSDB; AAB90781.
                                                                                                                                                                                                                                                                                     Nojima H, Yoshisue
Kuga T, Sekine S,
                                                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK. (NOJI/) NOJIMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                      02-CCT-2000; 2000WO-JP006840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WC200125427-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; shear stress-response protein; vascular disease; arteriosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH02904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH02904 standard; DNA; 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 489 BP; 130 A; 103 C; 134 G; 119 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ACATGCGTGAAGCAGGTG 139
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                                                                                                                                                                                                                                                                                     Obayashi M, Ota T,
amura Y, Sugano S;
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                                                                                                                                                                                                                                                                                                     Kawabata A,
                                                                                                                                                                                      disease caused by
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Query Match

30.0%;

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RESULT 12
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DR O7-NC
PR 18-DE
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                                                                                                                             Query Match
Best Local S
Matches 18
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Matches
                                                                                                                                                                                                                                                                                                     The present invention relates to novel differentially regulated genes and polypeptides encoded by them. Sequences of the invention are useful in diagnosing, staging, monitoring, prognosticating, preventing, treating or determining the predisposition to diseases or conditions such as prostate cancer. They may be used as molecular markers, drug targets, vaccines, in gene therapy, research, clinical medicine or forensic science. The present sequence is a differentially regulated prostate cDNA, Pc036-2 which codes for a pre-mRNA splicing factor. Pc036-2 gene is located on the prostate of the prostate of
                                                                                                                                                                                                                                  Sequence 1428 BP; 341 A; 296 C; 400 G; 391 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 29; Page 127-128; 100pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide for diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to, diseases conditions such as prostate cancer, and for research or forensic science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-NOV-2001; 2001US-0331041P.
07-NOV-2001; 2001US-0331042P.
18-DEC-2001; 2001US-0340251P.
07-JAN-2002; 2002US-0344791P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; differentially regulated protein; prevention; therapy; vaccine; prostate cancer; gene therapy; pre-mRNA splicing factor; Pc036-2; chromosome 17q21.3-q22; gene; ss.
                                                                                                                                                                                                                                                                                  chromosome 17q21.3-q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Pc036-2 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ORIG-) ORIGENE TECHNOLOGIES INC.
                                 543 ACATGCGTGAAGCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-449451/42.
)B; AAO29561.
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                                                                                                                                                            Similarity
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                                                                              ACATGCGTGAAGCAGGTG 58
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                                                                                                                                   Conservative
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                                                                                                                                                         Score 18; Fred. No.
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                                                                                                                                                                                DB 10;
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ADH28741
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                                                                                                                                                                                                                                                                                                                                          RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene marker.
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The invention relates to a method of classifying a cell sample as chronic phase chronic myelogenous leukaemia (CP-CML) or blast crisis CML (BC-CML). The method is useful for classifying a sample as CP-CML or BC-CML. The present sequence represents a human chronic myclogenous leukaemia (CML) gene marker used to distinguish blast crisis CML from chronic phase
Cytostatic; antidiabetic; anorectic; gynaecological; antipsoriatic; dermatological; antiarteriosclerotic; antiasthmatic; neuroprotective; nootropic; antiparkinsonian; nephrotropic; human; secreted protein; diagnostic; pharmaceutical; cancer; lung; oesophageal; liver; diabete;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Classifying cell sample as chronic phase chronic myelogenous leukemia or blast crisis chronic myelogenous leukemia by detecting difference in expression of genes corresponding to the markers such as X15415, U89436.
                                                                                                                                                                  Human secreted protein encoding DNA, seq id 141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1717 BP; 420 A; 343 C; 465 G; 489 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                        ADP07658 standard; DNA; 1926 BP
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st crisis CML; BC-CML; human; chronic myclogenous leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      515 ACATGCGTGAAGCAGGTG 532
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a human secreted polypeptide for diagnosing, preventing or treating disorders associated with the secreted proteins. The polypeptides and nucleic acid molecules of the invention are useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating a medical condition. These may be used for diagnosing, preventing or treating disorders related to the human secreted proteins, such as cancer (e.g. lung, cesophageal or liver cancer), diabetes, obesity, metabolic disorders, cardiovascular disorders, reproductive disorders, psoriasis, eczema, bronchitis, cystic fibrosis, atherosclerosis, benign prostatic hyperplasia, asthma, Alzheimer's disease, Parkinson's disease or renal disorders. Sequences given in records for ADP07528.ADP07709 represent human secreted protein encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUN-2002;
08-AUG-2002;
12-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA,
Birse CE,
tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell; colon; mouth; lung; prostatic; gynecological; human; gene; ds.
                                                HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ No 102
                                                                                                                                                                                                                                                                                                                                                                 Sequence 1926 BP; 479 A; 378 C; 568 G; 498 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; SEQ ID NO 141; 1157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human secreted polypeptides and nucleic acid molecules for diagnosing, preventing or treating disorders associated with the secreted proteins, such as cancer, diabetes, obesity, cardiovascular disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obesity; metabolic disorder; cardiovascular disorder; reproductive disorder; psoriasis; eczema; bronchitis; cystic fibrosis; atherosclerosis; benign prostatic hyperplasia; asthma; Alzheimer's disease; Parkinson's disease; renal disorder; gene; ds.
                                                                                  15-JAN-2004 (first entry)
                                                                                                                   ADD22452;
                                                                                                                                                    ADD22452 standard; DNA; 2765
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DB; ADP07840.
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2002US-0401157P.
2002US-0402585P.
2002US-0402799P.
2002US-0402799P.
2002US-0404959P.
2002US-0415902P.
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                30.0%; Score 18; DB 12; Length 1926; 100.0%; Pred. No. 5.6;
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R, Shi Y;
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Search completed: December 22,

2004, 22:44:12

Gaps

217.015 secs

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                                                                                                                                                                                                              The invention relates to a novel tumour antigenic peptide or polypeptide comprising a sequence selected from 99 sequences fully defined in the specification. The tumour antigenic peptide or polypeptide comprises a cc sequence selected from 99 sequences fully defined in the specification. Cc where the tumour antigenic peptide preferably has a sequence of Glu-Pro-Cc Pro-Leu-Ser-Glu-Glu-Thr-Phe, and the polypeptide preferably has a cc sequence comprising 393 amino acids fully defined in the specification. Cc The invention further provides a cancer vaccine comprising a tumour cc antigenic peptide or polypeptide, which has cytostatic activity. A tumour cc antigenic peptide, polypeptide, which has cytostatic activity. A tumour cc antigenic peptide, polypeptide, its encoding polymucleotide, a host transformed with the vector containing the cc polymucleotide, a host transformed with the vector or an antibody are compounds that interact with the tumour cantigenic peptide, the polypeptide or its encoding polymucleotide and cr or polymucleotide. The tumour antigenic peptide, the polypeptide or compounds that interact with the polypeptide cor polymucleotide. The tumour antigenic peptide, the polypeptide is useful for inducing cytotoxic T cells. The tumour antigenic peptide is coreal composition useful for treating cancer such as colon, mouth, lung, provides a contibodies. This polymosition useful for treating cancer. The tumour cantigenic peptide is create contibodies. This polymosition useful for treating cancer. The tumour cantigenic peptide is create contibodies. This polymosition useful for treating cancer. The tumour cantigenic peptide is create contibodies. This polymosic polymosition controlled is an antigen to create contribute in the polymosition useful for treating cancer is the bNA encoding one cantibodies.
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                                                                                                                                                                                                                                                               of the human tumour antigenic polypeptides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostatic or gynecological cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel tumor antigenic peptide or polypeptide useful for inducing cytotoxic T cells or for treating cancer such as colon, mouth, \Gamma
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509 ACATGCGTGAAGCAGGTG 526
                                                41 ACATGCGTGAAGCAGGTG 58
                                                                                                       18;
                                                                                                                                 Similarity
                                                                                                       Conservative
                                                                                                                              30.0%; Score 18; DB 10; Length 2765; 100.0%; Pred. No. 5.6;
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Result
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Maximum DB seq length: 2000000000
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-328-352-191
US-09-252-991A-8169
US-09-252-991A-993-5
US-08-48-199-5
US-08-48-199-5
US-08-767-333-9
US-09-316-601-2
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US-09-316-601-2
US-09-916-594-598
US-09-916-594-598
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Sequence 3335,
Sequence 18621, A
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Sequence 12, Appl
Sequence 11, Appl
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Sequence 7983, Ap
Sequence 8169, Ap
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Sequence	Sequence	Sequence	Sequence	Sequence		Sequence			Sequence	Sequence	æ			Sequence	w	Œ	Sequence
12926,	108, App	87, Appl	29234,	7, Appli	4894, A	810, App	27759,	2381, Ap	9517, A	2610, A	4877, Ap	957, Ap			76, App	528, App	9, Appl

ALIGNMENTS

RESULT 1 US-08-864-357F-7

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 60
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: primer sequence
US-08-864-357F-12
                                                                                                                                                                                 Sequence 12, Application US/08864357F
Patent No. 6255281
GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
ITILE OF INVENTION: Use of Recombinant Human Ute
ITILE OF INVENTION: Fibrotic Conditions
ITILE OF INVENTION: Fibrotic Conditions
ITILE OF INVENTION WIDER: US/08/864,357F
CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
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SEO ID NO 7
LENGTH: 60
TYPE: DNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: primer sequence
US-08-864-357F-7
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Patent No. 6255281

GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammato:
TITLE OF INVENTION: Pibrotic Conditions
FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
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US-08-864-357F-12/c
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100.0%; Pred. No. 2.5e-24;
tive 0; Mismatches 0;
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RESULT 5
US-09-023-655-504/c
; Sequence 504, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-1928
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US-09-328-352-1928
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SEQ ID NO 11
LENGTH: 59
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Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08864357F
Patent No. 6255281
GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammato
TITLE OF INVENTION: Fibroic Conditions
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1928
LENGTH: 624
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gary I. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                      177 CATGCGTGAAGCAGGT 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 AGGACATGCGTGAAGCAG 55
                                                                                                                                                                                                              42 CATGCGTGAAGCAGGT 57
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                                                                                                                                                                                                                                                    16;
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                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                        26.7%; Score 16; DB 4; 100.0%; Pred. No. 8.3;
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                                                                                                                                                                                                                                                                                               Length 624;
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7983
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                                                                                                                                                                                                                                                                                                                                          Sequence 7983, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                            SEQ ID NO 7983
LENGTH: 1959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                       APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27
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INFORMATION FOR SEQ ID NO: 504:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-(TELECOMMUNICATION INFORMATION:
                                                                                                         NUMBER OF SEQ ID NOS:
                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: TESTN
CLONE: 2006402
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TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION UNUBER: US/09/023,655
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear
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TYPE: nucleic acid
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8169
LENGTH: 2010
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US-08-472-217-1
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GENERAL INFORMATION:
APPLICANT: Alanen
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Patent No. 6551795
GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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APPLICANT:
                                                                                                                                                                                          STREET: 1100 CITY: Washington STATE: D.C.
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC COMPUTER:
COMPUTER: POLICY POLICY
CURRENT APPLICATION DATA;
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                        APPLICANT: Vihinen, Tapani
APPLICANT: W rri, Anni
TITLE OF INVENTION: Syndecan Stimulation Of Cellular
TITLE OF INVENTION: Differentiation
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 514
                APPLICATION NUMBER: FILING DATE: 07-JU
                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                 E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nilarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                        Mali, Markku
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Jaakkola, Panu
Jalkanen, Markku
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                     07-JUN-1995
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                                                                         Release #1.0, Version #1.25
                                 US/08/472,217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5851993
GENERAL INFORMATION:
APPLICANT: Jalkanen, Markku
APPLICANT: Mali, Markku
TITLE OF INVENTION: Suppression of Tumor Cell Growth
TITLE OF INVENTION: Syndecan-1 Ectodomain
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TELEPAX: (202) 371-540
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                      APPLICATION NUMBER: US/08/APPLICATION NUMBER: US/08/APPLICATION 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/APPLICATION NUMBER: US 08/APPLICATION NUMBER: US 08/APPLICATION NUMBER: Cimbala, Michele A.
                REGISTRATION NUMBER: 33,851
REFERENCE/DOKKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,199
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            STREET: LIVE
CITY: Washington
CHATE; DC
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1102.0050003
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US (
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: line: MOLECULE TYPE: DI HYPOTHETICAL: NO
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FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 26700 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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TELEFAX: 202-371-2540
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INFORMATION FOR SEC ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCY: 26700 base pairs
TYPE: nucleic acid

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STRANDEDNESS:

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INFORMATION FOR SEQ ID NO:
                                                                                                                 APPLICATION NUMBER: US 08/
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI
APPLICATION OF DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     ZIF: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                NAME: CIMBALA, MICHELB A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1708.0050004/MAC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
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APPLICANT: JAAKKOLA, PANU
APPLICANT: VIHINEN, TAPANI
TITLE OF INVENTION: SYNDECT
TITLE OF INVENTION: STIMUL!
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              TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/760,534A FILING DATE: 02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20005-3934
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23905..24040
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US-09-336-757-1
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APPLICANT:
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 26700 base pairs
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILLING DATE: 01-DEC-1993
ATTORNEY/AGENT INFORMATION:
NUMBER OF THE PARTY OF THE PARTY
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SYNDECAN ENHANCER ELEMENT AND SYNDECAN TITLE OF INVENTION: STIMULATION OF CELLULAR DIFFERENTIATION
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                                LOCATION:
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LOCATION:
LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                             NAME/KEY:
                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/336,757
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
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                                join(4378..4443, 22026..22106, 23001..23483, 23905..24039, 24251..24418)
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RESULT 13
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                                              RESULT 14
US-08-978-589A-1
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; OTHER INFORMATION: n means any nucleotide
US-09-270-767-18621
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US-09-270-767-3339
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 18661
LENGTH: 540
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 199-03-17
CURRENT FILING DATE: 199-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3339
LENGTH: 540
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Best Local S
Matches 16
Sequence 1, Application US/08978589A Patent No. 6087145 GENERAL INFORMATION:
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Patent No. 670349
                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                    ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                            Local Similarity
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                                                                                                              134 GCÁGCTATGGÁÁCTG 148
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16; Conservative
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                                                                                                                                                                             Conservative
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tive 0; Mismatches
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; TYPE: DNA
; ORGANISM: E, coli JM 109/pAL 612 strain
US-09-336-601-2
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                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1089
                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09336601
Patent No. 6184008
                                                                                                                 APPLICANT: OHTA, Hiromichi
APPLICANT: SUGAI, Takeshi
APPLICANT: SUGAI, Takeshi
APPLICANT: SISHII, Takeshi
APPLICANT: MITSUDA, Satoshi
TITLE OF INVENTION: PRODUCTION OF OPTICALLY ACTIVE SPHINGOID COMPOUND
FILE REFERENCE: 2185-349P
CURRENT APPLICATION NUMBER: US/09/336,601
CURRENT APPLICATION NUMBER: US/09/336,601
CURRENT FILING DATE: 1999-06-21
EARLIER APPLICATION NUMBER: 09/034,007
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 2
COUNTRIES FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 2
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Best Local (
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TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MULPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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ADDRESSEL:
ADDRESSEL:
STREET: P.O. BUA
CITY: PALLS CHURCH
STATE: VIRGINIA
""V; UNITED STATES OF AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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APPLICANT: MITSUDA, Satoshi
TITLE OF INVENTION: ESTERASE GENE AND ITS USE
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: DNA (genomic)
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FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Burckholderia cepacia STRAIN: SC-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O. BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 CGTGAAGCAGGTGCT 350
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15; Conserv
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100.0%; Pr
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Query Match
Search completed: December 23, 2004, 01:33:36

Query Matches

25.0%; Score 15; DB 3; Length 1089;
Best Local Similarity 100.0%; Pred. No. 30;
Mismatches 0; Indels 0; Gaps 0;
Mismatches 0; Indels 0; Gaps 0;

Mismatches 0; Indels 0; Gaps 0;

Mismatches 0; Indels 0; Gaps 0;

Mismatches 0; Indels 0; Gaps 0;

Mismatches 0; Indels 0; Gaps 0;

Mismatches 0; Indels 0; Gaps 0;

Mismatches 0; Indels 0; Gaps 0;
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Post-processing: Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 60.0 , Gapext 60.0
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397.214 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 2 US-09-898-616A-2

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Sequence 102427, Sequence 10327, A	quence 4830	Sequence 22078,	quence 739, Ar	duence 2183	equence 2182,	equence 28883,	equence 32178	e 3217	equence 50093	quence 50093,	equence 29863	equence 29862	equence 2986	equence 59300,	eguence s	equence 59298,	equence 29863	e 2986	equence 29862	equence 59300,	equence 59299,	equence 59298	nce 513, 🎜	equence 5226,	equence 9, App	e 231	e 1284,	equence 1284,	e 1284, 7	quence 10, Ap	equence 6, Ap

ALIGNMENTS

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WS-09-861-688-7

Sequence 7, Application US/09861688

Patent No. US20020173460A1

GENERAL INFORMATION: Use of Recombinant Human Uteroglobin in Treatment of TITLE OF INVENTION: Inflammatory and TITLE OF INVENTION: Fibrotic Conditions

FILE REFERENCE: 116142/2

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: 08/09/861,688

CURRENT FILING DATE: 1997-05-28

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.0

SEQ ID NO 7

OTHER INFORMATION: primer sequence

PERTURE:

OTHER INFORMATION: primer sequence

PERTURE:

OTHER INFORMATION: primer sequence

OF HACCAS Similarity 100.0%; Score 60; DB 9; Length 60;

Best Local Similarity 100.0%; Pred. No. 6.3e-24;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

I ACCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACCAGGACATGCGTGAAGCAGGTGCT 60

Db 1 AGCTACGAAGCAGCTATGGAACTGTTCTCTCCCGACCAGGACATGCGTGAAGCAGGTGCT 60
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                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Claragen Inc.
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00260
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR PILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00170
CURRENT PAPLICATION NUMBER: US/09/898,616A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR PILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Pilon, April
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OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                                 NAME/KEY: misc feature OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
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ORGANISM: Artificial Sequence
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1 AGCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACCAGGACATGCGTGAAGCAGGTGCT 60
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                                                                                                                Similarity
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                                                                                                             100.0%; Score 60; DB 15; 100.0%; Pred. No. 6.3e-24;
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  ; Sequence 7, Application US/09898616A; Publication No. US20030109429A1; GENERAL INFORMATION:
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US-09-861-688-12/c
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RESULT 6
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Publication No. US20040047857A1

GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH

ITTLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory

TITLE OF INVENTION: and Fibrotic Conditions

FILE REFERENCE: 116142-85

CURRENT APPLICATION NUMBER: US/10/647,371

CURRENT FILING DATE: 2003-08-25

PRIOR APPLICATION NUMBER: 09/549,926

PRIOR APPLICATION NUMBER: 09/549,926

PRIOR PRIOR DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.2

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09861688 Patent No. US20020173460A1 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/861,688
CURRENT FILING DATE: 2001-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment
TITLE OF INVENTION: Inflammatory and
TITLE OF INVENTION: Fibrotic Conditions
                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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100.0%; Pred. No. 6.3e-24;
                                                                                                                                                                                                   61.7%; Score 37; DB 9; Length 60; 100.0%; Pred. No. 6.3e-11;
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US-09-898-616A-7/c

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NAME/KEY: misc feature
OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
COTHER INFORMATION: d sequence maximized for expression in E. coli.
US-09-898-616A-7
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Best Local S
Matches 37
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APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment
TITLE OF INVENTION: Imflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00170
CURRENT APPLICATION NUMBER: US/09/898,616A
CURRENT APPLICATION NUMBER: US/09/898,616A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
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Publication No. US20030109429A1
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Best Local
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APPLICANT: Pilon, Aprile L
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REPERENCE: 116142/00170
CURRENT APPLICATION NUMBER: US/09/898,616A
CURRENT FILING DATE: 2002-10-15
                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
NTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
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                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
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37 AGCTACGAAGCAGCTATGGAACTGTTCTCTCCGGACC 1
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37; Conserv
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100.0%; Pred. No. 6.3e-11;
1tive 0; Mismatches 0;
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Pred. No.
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6.3e-11;
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RESULT 9
US-10-187-498A-8/c
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APPLICANT: Pilon, Aprile L
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 16142/00260
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PAtentIn version 3.1
SEQ ID NO 8
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APPLICANT: Pilon, Aprile L
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00260
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR PILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                FEATURE:
OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                          LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
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37; Conserv
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Pred. No. 6.3e-11;
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Query Match Best Local & Matches 3

Conservative

61.7%; Score 37; DB 15; Length 60, 100.0%; Pred. No. 6.3e-11; tive 0; Mismatches 0; Indels

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Gaps

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Best Local Similarity

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RESULT 12
US-09-898-616A-6/c
· sequence 6, Application US/09898616A
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US-09-861-688-11/c
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US-10-647-371-11/c
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US-10-647-371-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. US20020173460A1
GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment
TITLE OF INVENTION: Inflammatory and
TITLE OF INVENTION: Fibrotic Conditions
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SEQ ID NO 11
LENGTH: 60
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Publication No. US20040047857A1
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TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory
TITLE REFERENCE: 116142-85
CURRENT APPLICATION NUMBER: US/10/647,371
CURRENT FILING DATE: 2003-08-25
PRIOR APPLICATION NUMBER: 09/549,926
PRIOR APPLICATION NUMBER: 09/549,926
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 12
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CURRENT APPLICATION NUMBER: US/09/861,688
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
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OTHER INFORMATION: primer sequence
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ORGANISM: Artificial
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APPLICANT: Pilon, Aprile L
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/0260
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 59
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                                                                                                                                 Query Match
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APPLICANT: Weich, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00170
CURRENT APPLICATION NUMBER: US/09/898,616A
CURRENT FILING DATE: 2002-10-15
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                                                                                                                                                                                                NAME/KEY: misc_feature
OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
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OTHER INFORMATION: Ori
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                                           38 AGGACATGCGTGAAGCAG 55
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  59 AGGACATGCGTGAAGCAG
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9
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  42
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Pred. No.
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                                                                                          Mismatches
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Sequence 1284, Application US/09920300A

Patent No. US20020136728A1

GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Magher, Madeleine Joy
APPLICANT: M. Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FASESEQ FOR Windows Version 4.0
1ENGTH: 432
TYPE: DNA
CORRENT: AND SAPIENS
SEQ ID NO 1284
US-09-920-300A-1284
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Search completed: December 23, 2004, 05:19:26 Job time : 843.086 secs
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US-10-647-371-10/c
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US-09-920-300A-1284
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Publication No. US2004047857A1

GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory
TITLE PREPRENCE: 116142-85
FILE REPERENCE: 116142-85
CURRENT APPLICATION NUMBER: US/10/647,371
CURRENT FILING DATE: 2003-08-25
PRIOR APPLICATION NUMBER: 09/549,926
PRIOR APPLICATION NUMBER: 09/549,926
PRIOR TILING DATE: 2000-04-14
NUMBER OF SEQ ID NO5: 12
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
TENTUME EC
                                                                                                                                                                                                             Query Match 30.0%; Score 18; DB 9; Length 432; Best Local Similarity 100.0%; Pred. No. 3; Matches 18; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial
FEATURE:
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Database :
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop_60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 2 AR160920/c LOCUS DEFINITION	Ωy	Query Match Best Local Matches 5	ORIGIN	JOURNAL FEATURES Source	REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	RESULT 1 AR160917 LOCUS DEFINITION ACCESSION VERSION
AR160320.1 GI:16225993 Unknown. Unknown. Unclassified. 1 (bases 1 to 59) Pilon, A.L., Mukherjee, A.B. and Zhang, Z.	AR160920 59 bp DNA linear PAT 17-OCT-2001 Seguence 11 from patent US 6255281.	1 CAGCTGAAGAAACTGGTTGACACCCTGCCGCAGAAACCGCGTGAATCCATCATAAACTG 59	ch 100.0%; Score 59; DB 6; Length 59; l Similarity 100.0%; Pred. No. 3.3e-23; S9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="unknown" /mol_type="unassigned DNA"	and fibrotic conditions Patent: US 6255281-A 8 03-JUL-2001; Location/Qualifiers 159	Unclassified. 1 (bases 1 to 59) 1 (bases 1 to 59) Pilon, A.L., Mukherjee, A.B. and Zhang, Z. Use of recombinant human uteroglobin in treatment of inflammatory	Unknown: Unknown:	AR160917 Sequence 8 from patent US 6255281. AR160917 AR160917 AR160917.1 GI:16225984

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Biswald, K. Balari, J. Blankenburg, K. Byth, P. Brown, Bryant, N. Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V. Carter, K., Cavazos, I., Ceasax, H., Canderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasax, H., Canderon, E., Chen, C., Cockrell, K., Cox, C., Coyle, M., Cree, A., D. Souza, L., Chen, A., Chen, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D. Souza, L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Dapagado, O., Denson, S., Davrano, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duvul, B., Eaves, K., Egan, A., Bscotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Fraser, C.M., Halland, W., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hadann, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hiladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hiladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlabird, D., Jackson, A., Jackson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Hung, Z., King, L., Li, Z., Liu, J., Liu, Y., London, P., Longacre, S., Loyez, J., Lorensatewa, L., Louiseged, H., Lozado, R., J., Lu, X., Ma, J., Lowis, J., Liu, Y., London, P., London, P., Longacre, S., Loyez, J., Martin, R., Martin, R., Martinez, E., Manhauthew, J., Martin, R., Martin, R., Martinez, E., Manhauthew, J., Martin, R., Martin, R., Martinez, E., Martinez, S., John, M., Norris, K., Martin, R., Martinez, E., Morgan, M., Morris, K., Martin, R., Martinez, E., Martinez, E., Mortis, S., Manidasa, M., Murphy, M., Nair, L., Martinez, L., Petankoch, C., Petankoch, C., Petankoch, C., Petankoch, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., J., Resign, R., Shen, H., S
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37; Conser
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Ben
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Rattus norvegicus
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/mol_type="unassigned DNA"
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, assembly (a 'contig-scaffold'). Within each contig-scaffold, and sequence only sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Baylor Plaza, Houston, TX 77030, USA
1 (bases 1 to 62318)
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Submitted (11-OCT-2002) Human Genome Sequencing Center, Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by the finished sequence as soon as it is available and the accession number will be preserved.

1 62318: contig of 62318 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: XCYH

Center clone name: CH230-416G11

Center clone name: CH230-416G11

Assembly program: Phrap; version 0.990329

Consensus quality: 52773 bases at least Q40

Consensus quality: 53666 bases at least Q20

Consensus quality: 54142 bases at least Q20

Estimated insert size: 52859; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
/note="wgs_end_extension
clone_end:Sp6"_
complement(7376. .8361)
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                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref≈"taxon:10116"
                                                                                                                                                                                                                                                    'clone="CH230-416G11"
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/note="clone_boundary

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Best Local Similarity
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Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., De&rellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., 11ev,I., Johnson,R., Jones,C., Kamat,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
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AC117645

Mus musculus clone RP23-238F4, LOW-PASS SEQUENCE SAMPLING
AC117645

AC117645.5 GI:22549859

HTG: HTGS PHASEO.

Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                 Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (Dases 1 to 65394)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 65394)
Birren,B., Nusbaum,C.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus, clone RP23-238F4
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complement(54571. .55515)
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REFERENCE

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AC117645 LOCUS

KEYWORDS VERSION 밁 Ş ORIGIN

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McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Piere, K.L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (30-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 30, 2002 this sequence versible placed gi:22474966. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome_washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be preserved.
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Contact: sequence submissions@genome.wi.mit.edu

------Project Information

Center project name: L23887

Center clone name: 238_F_4
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                                                                                                                                                                                                                                                                                                                      COMMENT
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JOURNAL
MEDLINE
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Matches
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Best Local
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Liu,Y., Hu,X., Jia,P., Zhang,Y., Zhao,Q., Ying,K., Yu,S., Tang,Y.,
Weng,Q., Zhang,L., Lu,Y., Mu,J., Lu,Y., Zhang,L.S., Yu,Z., Fan,D.,
Liu,X., Lu,T., Li,C., Wu,Y., Sun,T., Lei,H., Li,T., Hu,H., Guan,J.,
Wu,M., Zhang,R., Zhou,B., Chen,Z., Chen,L., Jin,Z., Wang,R.,
Yin,H., Cai,Z., Ren,S., Lv,G., Gu,W., Zhu,G., Tu,Y., Jia,J.,
Zhang,Y., Chen,J., Kang,H., Chen,X., Shao,C., Sun,Y., Hu,Q.,
Zhang,X., Zhang,W., Wang,L., Ding,C., Sheng,H., Gu,J., Chen,S.,
Ni,L., Zhu,F., Chen,W., Lan,L., Lai,Y., Cheng,Z., Gu,M., Jiang,J.,
Li,J., Hong,G., Xue,Y. and Han,B.
Sequence and analysis of rice chromosome 4
L. Nature 420 (6913), 316-320 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group) oryza sativa (japonica cultivar-group) oryza sativa (japonica cultivar-group) Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
This is a complete sequence. Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan (http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (http://genemark.biology.gatech.edu/deneMark), tRNAscan-SE (Sean Eddy, http://genemark.biology.gatech.edu/ddy/ENAScan-SE/), searches of the complete sequence against NCBI none redundant protein database (nr
                                                                                                                                                                                                                                                                                                          Oryza sativa japonica (nipponbare) genomic DNA, chromosome clone: OSJNBa0067G20.
On Jul 8, 2003 this sequence version replaced gi:21740578.
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-SEP-2001) Han Bin, National Center for Gene Research, Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233, CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0067G20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence.
                                                                                                                                                                                                                                                            On Jul 8, 2003 this sequence version replaced gi:21740578 Web site: http://www.ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSJN00027
                                                                                                                                                                                                                           Assembly program: phrap
                                                                                                                                                                                                                                                                                                                                                                                                  bhan@ncgr.ac.cn
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45367: gap of 100 bp
46364: contig of 687 bp in
46154: gap of 100 bp
46866: contig of 712 bp in
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIKTCDSLIDDLRETFDNLRRYHLMINNEKCTPEVPSGKLLGFLVSGRGIEANPEKIK
ALENMKSPTRLKEVOKLIGCMAALSRFYARMGERGYBFLALKKOKFYWTQBABBAF
VALKRYLSNEPVLVAPOPUSELFLYLAFTYSVSTIIVEEREKVORPYYVSBALDBA
KTRYBOLOKLLYAVIMTSRKLRHYFQAHRVTVVSSFPLGEVVRNKDVVGRIAKMIVEL
SQFDVHFAFDAFTAAKSQVLADFVADWTNEDNKSDNOLDNETWTMAFDDOEKHVHHLNFR
VTNNTAEYEGLLARIFAAATLGVKRLIVKGASELVANOVHKDYKCSNPELSKYLVEVR
KLEKRFOGIEVHHYYRKUNIELDDLARRASROBEPLEGOTFLDILTREGVKEVGEVGEVSE
VTLDISSKATKAERAVADIETTDDWRFPLIKFINSEELPEDDTEAEKITRKAKIYCMV
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/db_xref="TIEMBL:Q7X665"
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MCVDYRALNEVTIKNKYPLPRIDDLFDQLKGATVFSKIDLRSGYHQLRIREEDIPKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNNLYKKAPNRVLLKSISSDNGRHLLLDIHEGIYGSHAAGWTLVGKAFRQGFFWPTTL
KYACDMVQRCEACQPHSKHTRLSAQALQTIPLTWPFSCWGLDILGPFPRGQGGYRFQF
VAIDKFTKWIEAVEWGEIKAVNAIKFIKGIFCRYGLPHRIITDNGSQFISADFQDYCI
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DNADVFAWQPSDMPGVPREACPKDHFPLARIDQLVDSTAGCELLSFLDAYSGYHQISM
AKEDBEKTTFITPFGVFCYVKMPPELITAGNTFQRTVQGALSDQLGNNVEAYVDDIVV
                             SPVLILPDTRKDFLVYCDASRQGLGRVLMQEAAVVHALKIWRHYLIGNRCEIYTDHKS
LKYIFTQSDLNLRQRRWLELIKDYDVRIHYHPGKANVVADPLSRKSHCNTLGVRGIPP
ELNQQMEALNLSIVGRGFLATLEAKPTLLDQIREAQKNDPDMYGLLKNMKQGKAAGFT
                                                                                                                              FTTRYGLYEFTVMSFGLTNAPAFFMNLMNKVFMEYLDKFVVVFIDDILVYSQSEEDHQ
QHLRLVLGKLREHQLYAKLRKCEFCLSBVKFLGHVISAKGVAVDFKTVTAVTDWKQPK
TVTQVRSFLGLAGYYRRFFENBSKIAQPMTQLLKKEEKFVMSPQCEKAFQTLKEKLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLGVKICFASVSHPQSNGQVERANGIVLQGIKTRVYDRLMSHDKKWVEELPSVLWAVR
TTPTTCNKETTFFLVYGSEAMLPSEL"
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/gene="CSJNBa0067G20.2"
complement (join')3453. .4786,4844. .5969,6199. .6561))
/gene="OSJNBa0067G20.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGGQDRRIQYWKTKFEVADLERTMLAVKKEQAVETLRGGEVWENSYLKSCCTSMARVORELRVPHGDPEESAAGYISWLNGACAQLDGVGKRIDEALKQECHRSSRYAGGHVLACLRDLREGFARSRRYPAEIDHLARNMAPFAEKIFQSMDWRWPSW"
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SGGTSGASPAAASTDVVLAPGSREVTPSGPVSDPAAGRGPLAAVLTWEDLQVEMGRLL
EASARGIGRDGRSRDVDDEDVQQRGQPEFEPHASPDNVDQTLATGPEMVTTSLDLESA
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SFIDIVDDLRVRGLSRYEVTADFVRRRIQPLQARVHPAFDYSGPEDATRVSPQGLNSE
TVGRRVGQVMISSPTTANIPVPLCEKRAAERDAAINALPLTNIIGPLADHQVAASLK
EDEHGTLWNGNRVCVPDDWELKQLILQEAHESSYSIHPGSTKIYLDLKEKYWWISMKR
                                                                                                                                                                                                                                                                                                                                                                                                                | gene="0SJNBa067G20.3" | (gene="0SJNBa067G20.3" | (codon start-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="OSJNBa0067G20.3"
join(6833. .7754,7830. .
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/db_xref="G1:38345107"
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/branslation="MAASHYAYQVLKMSGPKGTITIQGNTKLAVQCDKRSLDMVEQTP
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/translation="MEREAGGINPQPVLGRMVVIEDYILCDFIPPPSEFLLLVLNFYG
-SILHLMPNSIAFLSIFSHLCEAYIGVEPFLDLFRFYYELRMMENRVSGCVGFFLRD
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/db_xref="GI:38345106"
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1766. .1884,1983. .2473)
/gene="OSUNBA0067G20.1"
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(mol type="genomic DNA"
(cultivar="Nipponbare"
/sub_species="japonica"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="OSJNBa0067G20.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="OSJNBa0067G20.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon start=1
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                                                                                                                                                                                                                                                                                          IQLFAGHIIFSAEELGKKRYCKWHNSGSHSTNDCKVFRQQIQVAIEGGKIRFDDSKKF
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ADDNALANYLPTALKGSARSWLMHLLPYSISSWADLWQQFVANFQGTYKRHAIEDDLH
ALTQNSGESLREYVRRFNECRNTIPEITDASVIHAFKSGVRDCYTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLEDYGSSTTSALREVLAIDDVGTSARTNAEAENQLATPAQHIRAVNAILRETPYDPV
LNDDLARWTARLRESVTNLSNTFEEAAAAAHPEQPPTGDANAISEITSTAAERHDAHE
TMKIVPGVMSLHGAIMTKIEETAQTKTEAVITATTATITTIANGGCQTILVEDVAITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAD40482.1"
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HDLSSCKVLLSAMKAPPPKVQQSHIPIRDKDXERGATPTSDRFVGVIDIDPHEPSVLH
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/gene="OSJNBa0067G20.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNQILEDILRACVLNFGKTWDKSLPYAEFSYNNSYQASIQMAPYBALYGRKCQTFLLW
DQVGBSQVFGTDILREAEVKVRTIQENLKVAQSRQKSYADNRRRNLEFAVDNFVYLRV
TPLRGVHRFQTKGKLAPRFVGFFRIIARRGEVAYQLELPASLGNVHDVFHLSQLKKCL
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VVVDRLTKVARFIPVKTTYGGNKLAELYFARIKLQEELGTRLNFSTAYHPQTDGQTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLKVIPGTDAQDAQAIEEVEQIRQRAISAIQRYLSQ"
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/gene="OSJNBa0067G20.4"
/codon ביביד
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVPSEQADSEQIEVREDLTYVERPVKILDTMERRTRNRVIRFYKVQWSNHAEEEATWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(23570. .23705,23930. .24120,24214. .24858)
/gene="OSJNBa0067G20.7"
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RESULT 6
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VERSION
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      JOURNAL
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Matches 19; Conserv
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                                             Malen, C., Allen, H., Alsbrooks, S., Main, A., Angulano, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Main, A., Angulano, D., Allen, H., Alsbrooks, S., Main, A., Angulano, D., Anyalebeni, V., Ayyadi, A., Ayodei, M., Baca, E., Badden, H., Anyalebeni, V., Ayyadi, A., Ayodei, M., Baca, E., Badden, H., Baladwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Birwalo, X., Blair, J., Blandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Brynt, M., Bunay, C., Burch, P., Brown, M., Cree, A., D'Souza, I., Claveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, I., Claveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, I., Dayar, H., Dugar, Rocha, S., Denn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Escotto, M., Barnstead, M., Falis, T., Fan, G., Chen, Z., Core, C., Evan, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, M., Gerra, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, M., Guerra, M., Gerra, M., Gerra, M., Gerra, M., Gerra, M., Gerra, M., Harwey, Y., Havlak, P., Hawe, A., Hedreson, N., Hernandez, J., Harwey, Y., Havlak, P., Hawe, A., Hedreson, N., Hernandez, J., Harwey, Y., Havlak, P., Hawe, A., Hongson, A., Hogues, M., Hernandez, J., Harwey, Y., Havlak, P., Hawe, A., Hongson, A., Hogues, M., Harwey, S., Kelly, S., Kally, S., Kelly, S., Kally, S., Ka
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC111782,4
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TITLE
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On Nov 19, 2002 this sequence version replaced gi:23603299.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may excend beyond the ends of the clone and there may be sequence genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 232344)
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Center project name: GOCG
Center clone name: CH229-226/1
Center clone name: CH229-226/1
Assembly program: Phrap; version 0.990329
Consensus quality: 22573 bases at least Q40
Consensus quality: 224732 bases at least Q30
Consensus quality: 226208 bases at least Q30
Consensus quality: 225765; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226163
226263
230758
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                      /note="clone_boundary
clone_end:T7
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                                                                                                                                                     /note="wgs_end_extension clone_end:T7"
                                                                                                                                                                                                                                               /note="wgs_end_extension
clone_end:T7"
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/db_xref="taxon:10116"
/clone="CH230-226J1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
_sequence:BZ103653"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226162: contig of 226162 bp in length 226263: gap of unknown length 230757: contig of 4495 bp in length 230857: gap of unknown length 232344: contig of 1487 bp in length.
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Query Match
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Muzny, Dwarie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Alyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Biswalo, K., Blair, J., Bankenburg, K., Baristead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Byth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, M., Davis, C., Davy-Carroll, L., Dederich, D., Dederich, D., Davis, C., Davy-Carroll, L., Davis, M., Duyar, K., Davis, C., Finley, M., Flagy, M., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Gevara, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Gevara, M., Ghalard, M., Hamilton, C., Hamilton, C., Harrey, Y., Havak, P., Hawes, A., Henderson, M., Hernandez, J., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Hogues, M., Horlak, P., London, P., Longare, S., Lopez, J., Lowar, C., Karaft, C.L., Lebow, H., Levan, J., Lewis, L., Lewis, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191901 CTGAAGAACTGGTTGACA 191919
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Rattus norvegicus
Eukaryota; Metazoa; Chorda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus clone CH230-320L21, ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC128608.2 GI:22856092
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
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/note="wgs_contig"

226263. .227570

/note="wgs_contig"

227922. .230757
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224067. .226162
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100.0%; Pred. No.
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5.8;
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PROGRESS
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Center clone name: CH230-320L21
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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE

AUTHORS

RESULT 7 AC128608/c

DEFINITION

LOCUS

8

Best Loc Matches

ORIGIN

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Submitted (09-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2002 this sequence version replaced gi:21909412. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, C., Waldron, L., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, Yakub, S., Yen, J., Yoon, L., Yoon, V., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Yon Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 246787)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                      Center: Baylor College of Medicine Center code: Ed. Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 246787)
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be preserved
                                                                                                                                                                                                                                                                                                                                                                                                         245087
245187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.990329
Consensus quality: 219698 bases at least Q40
Consensus quality: 223003 bases at least Q30
Consensus quality: 224973 bases at least Q20
Estimated insert size: 239901; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimat
/note="wgs_contig"
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243322. .245086
                                                                                                                          54443.
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54443. .56179
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                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                            245086: contig of 245086 bp in length 245186: gap of unknown length 246787: contig of 1601 bp in length.
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A13578/c
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A13577
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KEYWORDS
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VERSION
KEYWORDS
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ORGANISM
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                                                                                         JOURNAL
                                                                                                                                                                ORGANISM
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                                                                        synthetic construct artificial sequences.

1 (bases 1 to 215)

Nygren,P.A., Abrahmsen,L. and Uhlen,M.

A recombinant fusion protein, its use and a recombinant vector Patent: EP 0333691-A 2 20-SEP-1989;
CEMU BIOTEXNIK AB
                                                                                                                                                                                                          A13578.1 GI:489637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetic construct artificial sequences.

1 (bases 1 to 215)

1 (pases 1 to 215)

Nygren,P.A., Abrahmsen,L. and Uhlen,M.

A recombinant fusion protein, its use and a recombinant vector Patent: EP 0333691-A 1 20-SEP-1989;

CEMU BIOTEXNIK AB
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                                                                                                                                                                              synthetic construct
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A13577
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Conservative
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                                                                                                                                                                                                                                     gene.
/organism≈"synthetic construct"
/mol_type≈"unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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/proteim_id="CAA01122.1"
/db xref="GI:491683"
/translation="WAYRPSETLCGGELVDTLQFVCGDRGFYFSRPASRVSRRSRGIV
EECCFRSCDLALLETYCATPAKSE"
                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="synthetic construct"
mol_type="unassioned מאין"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="IGF II"
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100.0%; Pred. No.
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AK073198.1 G1:32983221
FLI_CDNA; CAP trapper.
oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group) cDNA clone: J033022I15,
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                     The Rice Full Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Ooka,
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AK073198
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1 (bases 1 to 220)

Easton,A.M., Gierse,J.K., Seetharam,R., F

Production of bovine insulin-like growth

Escherichia coli
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.
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/trans1_table=1
/product='nsulin-like growth factor 2"
/protein_id="AAA72971.1"
/protein_id="AAA72971.1"
/db_xref="GI:208030"
/translation="MAXRPSETICGGELVDTLQFVCGDRGFYFSRPSSRINRRSRGI/LECCFRSCDLALLETYCATPAKSE"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Obtsuki, K., Shishki, T., Foundation of Advancement of International Science Genome Sequencing & Ambuscheric Group, Comon, Y., Whrekami, K., 11da, Y., Sigano, S., Pojimura, T., Shraki, V., Tgunoda, Y., Kirosaki, T., Kodama, T., Kobayashi, M., Xiso, O., Lu, M., Nariakas, R., Sugiyama, A., Miruno, K., Yokomizo, S., Mikura, J., Keda, R., Sigiyama, A., Miruno, K., Yokomizo, S., Mikura, J., Keda, R., Sigiyama, A., Miruno, K., Yokomizo, S., Mikura, J., Kada, R., Sigiyama, A., Miruno, K., Yokomizo, S., Mikura, J., Kada, R., Sigiyama, A., Miruno, K., Yokomizo, S., Mikura, J., Kada, R., Sigiyama, A., Miruno, K., Yokomizo, S., Mikura, J., Kada, R., Kada, J., Gasaki, D., Galeri, M., Matsuka, R., Kohayashi, K., Kada, A., Hashidama, Y., Rayashi, Y., Matsuka, K., Shinagawa, J., Shixaki, T., Yoshino, M., and Hayashizaki, Y., Babkaka, K., Shinagawa, J., Shixaki, T., Yoshino, M., and Hayashizaki, Y., Hayashi, K., Salaki, M., Salaki, K., Salaki,
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COMMENT

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REFERENCE AUTHORS

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AKO65797.1 GI:32975815
FILI_CDNA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi.S., Satoh.K., Nagata,T., Kawagdashira,N., Doi.K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohteda,E., Yahagi,W., Suzuki,K., Li,C., Chenki,K., Shishik,J., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoters for regulation of plant gene expression Patent: WO 0198480-A 235 27-DEC-2001; Syngenta Participations AG (CH)
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                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group) cDNA clone:J013041K05,
                                                                                                                                                                                                                                                                                                                                                                                                                    AK065797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Budworth, P., Brown, D., Chang, H.S., Zhu, T., Han, B., Wang, X. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX461306.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"

"mol type="mRNA"

/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="J033022I15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.5%; Score 18; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                    3176 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 2004; 24;
                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                    PLN 24-JUL-2003
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REFERENCE AUTHORS

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FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., FAIS Genome Sequencing & Analysis Group: Otomo, Y., Tida, Y., FAIS Genome Sequencing & Analysis, T., Kusumagi, T., Kusumagi, T., Lu, M., Masuda, H., Miura, J., Kodama, T., Kususaki, T., Kusumagi, T., Lu, M., Masuda, H., Miura, J., Oka, M., Ryu, R., Sugano, S., Sugiyanma, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Maise, Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken, Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, M., Hiramoto, K., Itoh, M., Kagawa, I., Kanagawa, S., Katch, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sasaka, T., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Shiraki, F., Yasunishi, A. and Hayashizaki, Y. Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiracka, T., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiracka, T., Idda, Y., Ikeda, R., Imamura, K., Imotani, K., Ishikiki, J., Ishi, Y., Ishikawa, M., Itch, M., Kagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa, Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Koya, S., Kurishara, C., Kurosaki, T., Xusumegi, T., Li, C., Lu, M., Koya, S., Kurishara, K., Matsuyama, T., Miura, J., Myazaki, A., Mazuho, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Maniki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Ogato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimara, A., Takahashi, F., Takaki, K., Xie, O., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (05-DEC-2001) Shoshi Kikuchi, National İnstitute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8802, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iida,Y., Sugano,S., Pujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Mikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:,
Kawai,J., Carninoi,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y., Shinagawa,A., Shiraki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,T., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    URL : http://cdna01.dna.affrc.go.jp/cDNA/
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Location/Qualifiers
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AUTHORS
TITLE
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M33799.1 GI:151627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 7419)
Bssar, D.W., Eberly, L. and Crawford, I.P.
Bssar, D.W., Eberly, L. and Crawford, I.P.
Evolutionary differences in chromosomal locations of four early
genes of the tryptophan pathway in fluorescent pseudomonads: DN;
sequences and characterization of Pseudomonas putida trpE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    з остоласластсства 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Original source text: P.putida (strain ATCC 232287) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas putida
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anthranilate synthetase; indoleglycerol phosphate synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 172 (2), 867-883 (1990)
                                                                                                                                                                                                                                                      EHLMLIDLGRNDVGRVSSTGSVRLTEKNVIERYSNVMHIVSNVAGQLREGLTAMDALR
AILPAGTLSGAPKIRAMEIIDELEPVKRGVYGGAVGYFAMNGNMDTAIAIRTAVINDG
                                                                                                                                                                                                                                                                                                             DNLAGKMHA I VI VDPAEEQAFEQGQARLQGILLETIRQPI TPRRGLDI.SGPQAAEPEFR
SSYTREDYENAVGRIKEY I LAGDCMQVVPSQRMS I DFKAAP I DLYRALRC FNPTPYMY
FFNFGDFHVVGSSPEVI VR VEDNI VTVR PI AGTR PRGATEBADRALEDDILISDIKEI A
                                                                                                                                                                                                                                                                                                                                                                                                         /product="anthranilate synthetase alpha-subunit"
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/mol_type="mRNA"
/cultivar="Mipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
translation="MSETYPVLIVSKLLMRVIKAHARWRWRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="trpE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="trpE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="ATCC 232287"
/db_xref="taxon:303"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="J013041K05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         table=11
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     REFERENCE
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                                                                                                                                         REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                            ACCESSION
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                JOURNAL
                                                                                                               AUTHORS
                                                                                                                                                                                                                                               ORGANISM
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                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotts; core eudicotts; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 42499)
1 (bases 1, Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Sykes, S.M., Kaull, S., Mason, T.M., Kerlavage, A.R., Adams, M.D., Somerville, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                           AC004625 42499 bp DNA linear PLN 11-MAR-2002 Arabidopsis thaliana chromosome 2 clone T26013 map CICI1C08,
     Unpublished 2 (bases 1
                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                       HTG
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                                                                                                                                                                                                                                                                                                                              AC004625.3 GI:20197200
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  (bases 1 to 42499)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSVPTVLERIIARKFQEVAERSARVSLAELERLAKTADAPRGFA NALIEQAKRKQPAVIAEIKKASPSKGVLREHFVPAEIAVSYEKGGATCLSVLTIVDVPF GOADEYLQQARAVSLEVIRKOPMVDY9IVBARALGADCVLLIVSALDDVKWAELAA GAADEYLQQARAAVSLEVIRKDPMVDF9IVGVNNRNLHTFEVSLETTLDLLPRIPRI PRD RAAITESGILNRADVELMAINEVYSFLVGEAFWRAEQFGLELQRLFFPEQVKXTVQPL D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MDIKSALSRIVGQLDLTTEEMRDVMRQIMTGQCTEAQIGAFLMG

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VHSKDGLDEFSLAAPTFVAELKNGBITEYMVEPEDLGMKSQSLHGLAVENPQASLEL

LTDALGERKTENGGKAAEMIVLNAGAALYAADHAMTLAQGVELAHDVLHTGLAWEKLQ

LTDALGERKTENGGKAAEMIVLNAGAALYAADHAMTLAQGVELAHDVLHTGLAWEKLQ
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berivvsegecteseadysieallhfagterilgvcledgesigaeggdvvraegymh
gktespyhhrdlgvftglinplivtryhslivvkeetledclevtawtahedgsvdeimg
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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3 (bases 1 to 42499)
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Direct Submission
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  8261. .8300 Trich"
/rpt family="AT rich"
complement(8423. .8563)
/rpt family="AT rich"
complement(8590. .8611)
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/note="synonym: T26J13.3; predicted by genscan"

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9516. 9615,9739. 9789,10210. 10289,10327. 10421,
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/note="overlap with BAC clone F13H10 (AC005662:1. .5112)."
                                                                                                                                                                                              RRMNGRQLDGVGVRDRFFFFGYRVYSDRRLRTIRVF"
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/rod>~~ ~*
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|mol type="genomic DNA"
|cultivar="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="At2g41440"
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                                                                                                                                      rpt_family="AT_rich"
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getestilkelvpvkgrkgelistlrihmdsnipdgketssstrbsdyttakkisne

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KVMTMNVNGLRGLLKFESFSALOLAQRENFDIILLQETKLQVKDVEEIKKTLIDGYDH

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SGDGLKRLSYRIEEMDRTLSNHIKELEKSKPVVLTGDLNCAHEEIDIFNPAGNKRSAG
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                                                                     complement (25382. .29598)
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                                                                                                                                                      complement (24160. .24183)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(18968. 19020,19356. 19536,19634. 19728,19855. 19934,
20201. 20419,20513. 20835,20937. 21047,21199. 21266,
21163. 214410,21494. 21574,21652. 21811,21885. 22206)
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jeane="At2941460"
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SLRNLLRDVPADVDEVIFTNYESVYERDDIKEPFTEVSMFKKNFKHLPREVYYGNYKE
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SDLTSRRDRGGCKPTKKDVKRCEMLDFDRAAFIIASTSTSEEMLQWYRERVVWTDDNL
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6. .17234,17326. .17460,17549. .17593,17684. .17871,
0. .18101,18181. .18324)
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Search completed: December 22, 2004, 23:36:38 Job time: 841.543 secs
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Best Local
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                                                                                                                                                                                                                                      Similarity
                                                                                                                                                   GCAGAAACCGCGTGAATC 47
                                                                                                                                                                                                            Conservative
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EELANRFEEEDVQLLRVLQQQLREKVERLRFLIKRWTGKDDDAHFTELQALESRLKDV
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s. .32014))
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Maximum DB seq length: 2000000000
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59
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	80	ID	Description
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N	59	100.0	59	12	ADL27628	Adl27628 Recombina
c 3	37	62.7	59	9	ABZ58375	Abz58375 Human ute
0 4	37	62.7	ទ	12	ADL27631	Adl27631 Recombina
ហ	18	30.5	215	Ь	AAN90906	Aan90906 Synthetic
ი თ	17	28.8	195	6	ABK76145	Abk76145 Bacillus
c 7	17	28.8	993	10	ADC24050	
	17	28.8	993	12	ADH36151	
ი 9	17	28.8	993	12	ADG93852	
c 10	17	28.8	993	12	ADI62449	
c 11	17	28.8	993	12	ADI64570	
12	17	28.8	3530	4	ABL08480	Dros
Д	17	28.8	5568	10	ABX08140	Abx08140 S. pneumo
<u></u>	17	28.8	5568	12	ADM91810	Adm91810 s pneumon
c 15	17	28.8	14736	N	AAV52304	Aav52304 Streptoco
c 16	17	28.8	62598	10	ABS56454_21	Continuation (22 o
c 17	16	27.1	60	9	ABZ58374	Abz58374 Human ute
c 18	16	27.1	60	12	ADL27630	Adl27630 Recombina
19	16	27.1	311	4.	AAL01419	Aal01419 Human rep
20	16	27.1	377	œ	ABX55377	Abx55377 Bovine ES
2	16	27.1	603		7 1 2 2 2 2 2 2 2	かかぶつ4549 ひっちょうへのつ

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21469	11204	11204	10327	6564	5603	4221	3163	3108	3056	2874	2743	2659	2658	2658	2658	2142	1769	1346	933	743	667	659	639
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956	ABS73286	w	53	AAC55314	ABL12539	ADO57346	ADE25034	ABL24046	AAC42758	ACA18781	ADB68899	AAS88462	AAS73288	AAS94408	AAS90260	ABD02265	ABN98233	AAS73783	ABD02206	ADB69260	ABQ75940	AAF08058	ADB69621
68 Hum	Abs73286 DNA encod	339	Abl12538 Drosophil	314	Abl12539 Drosophil	Ado57346 DNA encod	-	Abl24046 Drosophil	Aac42758 Arabidops	Acal8781 Prokaryot				Aas94408 DNA encod	Aas90260 DNA encod	Abd02265 Pseudomon	Abn98233 Arabidops	Aas73783 DNA encod		Adb69260 C. neofor	Abq75940 CHD activ	Aaf08058 Fusarium	Adb69621 C. neofor

ALIGNMENTS

RESULT 1
ABZ58372
ID S8372
AC ABZ5
XX ABZ5
AC ABZ5
XX Huma
XX Huma
XX Huma
KW anti
KW anti
XX Synt
XX Synt
XX I6-J
XX O2-J
XX O2-J
XX PF 02-J
XX WP1;
XX Pilo
DR WP1;
XX Pilo
DR WP1;
XX Pilo
CC Cong
CC Gasse
CC (huge
CC Comp Pilon AL, 02-JUL-2002; 2002WO-US020836. Homo sapiens. Synthetic. antiarthritic; Human; uteroglobin; respiratory distress; antiinflammatory; antifibrotic; 28-APR-2003 (first entry) ABZ58372 standard; DNA; 59 BP 02-JUL-2001; 2001US-00898616 16-JAN-2003. W02003003979-A2 antiinflammatory; antiasthmatic; nephrotropic; antirheumatic; Human uteroglobin synthetic gene oligonucleotide 3. ABZ58372; (CLAR-) CLARAGEN INC. Welch RE;

Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic gene which codes for human uteroglobin.

WPI; 2003-221527/21.

Claim 1; Page 33; 127pp; English.

The present sequence is that of oligonuclectide 3, which was used in the construction of a synthetic gene for the production of human uteroglobin (hUG) in bacteria. Oligonuclectides 1-4 (see ABZ58370-73) were used to assemble the coding strand and oligonuclectides 5-8 (see ABZ58374-77) the complementary strand. The gene was assembled by annealing and ligation of the oligonuclectides. Because mature native hUG has glutamic acid at its N-terminus, an initiator methionine was added to the N-terminus, and

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RESULT 2
ADL27628
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of recombinant human uteroglobin (rhUG), comprising a synthetic gene or human cDNA sequence which codes for human UG, constructed from the oligonucleotides appearing as ADL27626-ADL27629, and which further comprises Net-Ala Ala at the N-terminus of the sequence. Also included are producing an rhUG master cell bank (comprising inoculating a suitable incubating broth with an aliquot portion of a rhUG research seed bank to form a bacterial culture, incubating the bacterial culture, adding a cryopreserved to the bacterial culture to form a cryopreserved solution, transferring a portion of the cryopreserved solution to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon usage was optimised for expression in bacteria. In an example from the invention, the synthetic gene was cloned into plasmid pCG12 (see ABZ58378) and recombinant bUG (see ABP72259) was produced in Escherichia coli strain CG12. The invention relates generally to the production of recombinant bUG by bacterial expression, protein purification and scaled-up production according to current good manufacturing practices. The recombinant bUG is useful for the treatment of inflammatory and fibrotic conditions, such as neonatal respiratory distress syndrome and conditions, such as neonatal respiratory distress syndrome and bronchopulmonary dysplasma. It may also be used to treat conditions as the conditions are conditions as the conditions are conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial expression system for production of recombinant human uteroglobin comprising synthetic gene or human cDNA sequence which codes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MELC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; recombinant human uteroglobin; rhUG;
bacterial expression system; rhUG master cell bank;
rhUG research seed bank; anti-inflammatory; secretory phospholipase A 2;
fibronectin; respiratory distress; inflammation; fibrotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-1997; 97US-00864357.
02-JUL-2001; 2001US-00898616.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59 BP; 19 A; 17 C; 13 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                           The invention relates to a bacterial expression system for the production
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-051527/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for human uteroglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
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WELCH R W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 welch RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human uteroglobin, rhUG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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CC cryovial and storing the cryovial at a temperature below -60 degrees C), CC expressing rhUG (comprising providing a production seed cell bank culture comprising an expression vector capable of expressing rhUG, inoculating a CC inoculating a large scale fermenter with the inoculum formed from the continue within the large scale fermenter with the inoculum formed from the collure within the large scale fermenter, adding an induction agent to culture within the large scale fermenter, adding an induction agent to conture within the large scale fermenter, adding an induction agent to the fermentation culture to induce the expression of rhUG and harvesting the above fermentation culture), purifying rhUG, determining the potency cof rhUG in a sample, measuring in vitro anti-inflammatory effect arising from inhibition or blocking of secretory phospholipase A 2 enzymes by purity of rhUG, and a pharmaceutical composition comprising a purified crhUG and a carrier or diluent. The bacterial expression system is useful for producing a rhUG research seed bank or a pharmaceutical grade rhUG distress. The rhUG is useful for treating inflammation and fibrotic construct the synthetic rhUG gene.
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Query Match
Best Local :
                                                              Sequence 59 BP; 19 A; 17 C; 13 G; 10 T; 0 U; 0 Other;
             100.0%;
Score 59; DB 12;
Pred. No. 7.3e-22;
; Mismatches 0;
                              Length 59
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Similarity

Conservative

0

Indels

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Gaps

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밁 8 CAGCTGAAGAAACTGGTTGACACCCTGCCGCAGAAACCGCGTGAATCCATCATAAACTG CAGCTGAAGAACTGGTTGACACCCTGCCGCAGAAACCGCGTGAATCCATCATAAACTG 69

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ABZ58375/c
ABZ58376/c
ID ABZ583
XX
AC ABZ583
XX
AC ABZ583
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AC ABZ583
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Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABZ58375 standard; DNA; 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Human uteroglobin synthetic gene oligonucleotide 6.

antiarthritic; ss. antiinflammatory; Human; uteroglobin; antiasthmatic; nephrotropic; antirheumatic; respiratory distress; antiinflammatory; antifibrotic;

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WO2003003979-A2
                            Synthetic
                                          Homo sapiens
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02-JUL-2001; 2001US-00898616 02-JUL-2002; 2002WO-US020836 16-JAN-2003

WPI; 2003-221527/21. (CLAR-) CLARAGEN INC P Welch RE

Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic gene which codes for human uteroglobin.

Example 1; Page 33; 127pp; English.

The present sequence is that of oligonucleotide 6, which was used in the construction of a synthetic gene for the production of human uteroglobin (hUG) in bacteria. Oligonucleotides 1-4 (see ABZ58370-73) were used to assemble the coding strand and oligonucleotides 5-8 (see ABZ58374-77) the

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ADL27631/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local !
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The invention relates to a bacterial expression system for the production of recombinant human uteroglobin (rhUG), comprising a synthetic gene or human cDNA sequence which codes for human UG, constructed from the oligonucleotides appearing as ADL27626-ADL27629, and which further comprises Met-Ala-Ala at the N-terminus of the sequence. Also included are producing an rhUG master cell bank (comprising inoculating a suitable incubating broth with an aliquot portion of a rhUG research seed bank to
                                                                                                                                                                                                                                                                                                                                                                                           Bacterial expression system for production of recombinant human uteroglobin comprising synthetic gene or human cDNA sequence which codes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-1997; 97US-00864357.
02-JUL-2001; 2001US-00898616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; recombinant human uteroglobin; rhUG;
bacterial expression system; rhUG master cell bank;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-2004
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                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 6; 64pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rhUG research seed bank; anti-inflammatory; secretory phospholipase A 2; fibronectin; respiratory distress; inflammation; fibrotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant human uteroglobin, rhUG, non-coding oligonucleotide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PILO/) PILON A L. (WELC/) WELCH R W.
                                                                                                                                                                                                                                                                                                                                                                human uteroglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑĹ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59
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В Š

New recombinant fusion protein comprising desired protein - flanked by IgG-binding domain of staphylococcal protein A and albumin-binding domain of streptococcal protein G.

Synthetic IGF-II was constructed from 22 oligonucleotides.

The gene was

Disclosure; Fig 1; 10pp; English.

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RESULT 5
AAN90906
ID AAN9
AC AAN9
AC AAN9
AC Synt
XX Ep32
XX Ep32
XX Ep32
XX IP-N
XX I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic IGF-II; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic human IGF-II.
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                                                                                                                                                                                                                                                                                                                                                      Nygren PA,
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26-JAN-1990
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                                                                                                                                                                                                                                                          P-PSDB; AAP91389.
                                                                                                                                                                                                                                                                                            WPI; 1989-272436/38.
                                                                                                                                                                                                                                                                                                                                                                                                                (CEMU-) CEMU BIOTECHNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-1988;
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                                                                                                                                                                                                                                                                                                                                                      Abrahmsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
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100.0%;
                                                                                                                                                                                                                                                                                                                                                      Uhlen M;
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Pred. No.
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The invention describes a method of monitoring differential expression of CC genes in a first Bacillus cell relative to expression of the genes in cother Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining crelative gene expression by an observed hybridisation reporter signal of CC a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes coin one or more second Bacillus cells. The method is useful for monitoring CC global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and compitoring gene copy number variation and stabilty. Monitoring changes cin expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, converses or other physiological provocation. Extensive follow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                      Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-2000; 2000US-00680598.
27-MAR-2001; 2001US-0279526P.
                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 3436; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    physiological provocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Differential gene expression; genomic sequenced tag; GST altered culture condition; environmental stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus licheniformis genomic sequence tag
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Pred. No. 8.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                       21-JUN-2001; 2001US-0300189F
30-JUL-2001; 2001US-0309006F
22-JAN-2002; 2002US-0351336F
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                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                               enantiomer; chiral medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; ds; nitrilase; nitrile; cyanohyrdin; ammonia; biocatalyst;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence (SeqID 317) encoding a nitrilase enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 195 BP; 34 A; 48 C; 56 G; 57 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               15-MAY-2002; 2002WO-US015983
                                                                                                                                                                                                                                                                                          (DIVE-) DIVERSA CORP. (MADD/) MADDEN D.
                                                                                                                                                                                                                                         2003-201417/19
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Burk M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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100.0%; Pred. No.
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Novel nitrilase polypeptide, useful for making (R)- or 3-hydroxybutyric acid or (R)- or (S)-mandelic acid or (S) actic acid derivative and for producing pharmaceutical c (S)-ethyl-4-cyano
(S)- or (R)-phenyl
al composition, and

Claim 1; SEQ ID NO 317; 560pp; English.

This invention relates to nitrilases and the nucleic acids that encode these enzymes thereof. Specifically, it refers to polypeptides that exhibit nitrilase activity, i.e. the ability to directly hydrolyse nitriles or cyanohyrdins into their corresponding carboxylic acids and ammonia. Nitrilases have commercial utility as biocatalysts for use in the synthesis of enantiomerically pure aromatic and alighatic amino acids, as well as hydroxy acids, which are important for the development of chiral medicines. Furthermore, the present invention describes nitrilases, isolated from mesophila microorganisms, that have improved activity and stability at increased pH and temperature. They are also inexpensive, efficient catalysts, have broad substrate specificity and are capable of chiral differentiation. This polynuclectide is a DNA sequence that encodes a nitrilase enzyme of the invention.

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Sequence 993

B₽;

188

A; 330

C; 305 G; 170 T; 0 U; 0 Other;

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ADH36151/c
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Matches 17
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Best Local
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                                                                                                                                  This invention relates to a novel method of monitoring chemical or biochemical processes. The method involves providing a reactant comprising cyanide (or a material that can be converted to a cyanide) that generates as a reaction product cyanide or a material that can be converted to cyanide and measuring the concentration of produced cyanide. The method is useful for monitoring a chemical or biochemical process. The method is effective for high throughput systems and is sufficiently sensitive to detect a small amount of product. The present sequence is that of a gene which encodes a nitrilase enzyme which can be used in the method of the invention.
                                                                                                                                                                                                                                                                                                                      Monitoring a chemical or biochemical process comprises providing a reactant comprising a cyanide or a material that can be converted to cyanide or a reactant that generates a cyanide or a material that can converted to cyanide.
                                                                                                          Seguence 993 BP; 188 A; 330 C; 305 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           Claim 74; SEQ ID NO 317; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcquaid J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2003; 2003WO-US015639.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemical process monitoring-related nitrilase gene sequence SeqID317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weiner D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  high throughput system; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemical process monitoring; biochemical process monitoring; cyanide;
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860 CCGCGTGAATCCATCAT 844
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                           CCGCGTGAATCCATCAT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaplin JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Stege J;
                                                   Conservative
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                                             28.8%; 50.
100.0%; Pr/
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                                                   Score 17; DB; Pred. No. 30
0; Mismatches
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Pred. No.
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RESULT 9 ADG93852/c

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RESULT 10
ADI62449/c
ID ADI62449/c
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DT 22-APR
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Best Local &
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                           (R)-ethyl 4-cyano-3-hydroxybutyric acid; epichlorohydrin; 3-hydroxyglutaronitrile; 3-hydroxyglutaronitrile; 4-cyano-3-hydroxybutyric acid; ethyl-4-cyano-3-hydroxybutyric acid; ethyl-4-cyano-3-hydroxybutyric acid; mixed hyperlipidaemia; homozygous familial hypercholesterolaemia; antilipaemic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention is related to a novel isolated or recombinant nucleic acid encoding a protein having nitrilase activity. Nitrilase's are capable of converting nitrile's directly to carboxylic acids and have great potential for use in industrial chemical processes. The isolated nitrilase proteins of the invention have increased activity and stability at increased pH and temperature when compared to those conventionally
   Unidentified
                                                                                                                                                                                                            ADI62449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used. In addition, the nucleic acid of the invention is useful for screening enantioselective transformation. The present sequence is that of a DNA sequence which encodes a nitrilase enzyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nitrilase activity, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nitrilase; nitrile; carboxylic acid; chemical process; pH; enantioselective transformation; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nitrilase enzyme gene sequence
                                                                                                                                          DNA encoding nitrilase polypeptide #159.
                                                                                                                                                                             22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated or recombinant nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desantis G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-2002;
09-SEP-2002;
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                                                                                                             Atorvastatin; (R)-ethyl 4-cyano-3-hydroxybutyrate;
                                                                                                                                                                                                                                         ADI62449 standard; DNA; 993 BP
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                                                                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; SEQ ID NO 317; 295pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                       CCGCGTGAATCCATCAT
                                                                                                                                                                                                                                                                                                                                                     CCGCGTGAATCCATCAT 53
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 188 A; 330 C; 305 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Short JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002US-00146772
2002US-00241742
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
30;
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RESULT 11
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for preparating an atorvastatin intermediate known as (R)-ethyl 4-cyano-3-hydroxybutyrate ((R)-ethyl 4-cyano-3-hydroxybutyrate (R)-ethyl 4-cyano-3-hydroxybutyric acid). The method comprises optionally converting epichlorohydrin or equivalent to 3-hydroxyglutaronitrile, catalytic conversion of 3-hydroxyglutaronitrile or equivalent to 4-cyano-3-hydroxybutyric to ethyl-4-cyano-3-hydroxybutyric converting 4-cyano-3-hydroxybutyric to ethyl-4-cyano-3-hydroxybutyric acid, and converting this to (R)-ethyl 4-cyano-3-hydroxybutyrate. The method involves whole cell processes, cell lysate process, "one por processes, and "multi-pot" processes using a variety of parameters. Atorvastatin is used, in conjunction with dietary restriction, in the management of hyperlipidaemia, including hypercholesterolaemia. The present sequence encodes a nitrilase polypeptide obtained from an environmental
                                                                                                                                                                                         (R)-ethyl 4-cyano-3-hydroxybutyric acid; nitrile hydrolysis; carboxylic acid; cyanohydrin moiety hydrolysis; aminonitrile moiety hydrolysis; chiral alpha-hydroxy acid molecule; chiral amino acid molecule; (S)-ethyl 4-cyano-3-hydroxybutyric acid; (R)-mandelic acid; (S)-mandelic acid; (S)-mandelic acid; (S)-phenyl lactic acid derivative; (R)-phenyl lactic acid derivative;
      US2004014195-A1
                                                                    Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI64570 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding nitrilase seq id 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADI64570;
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28-JUN-2002; 2002US-0392944P.
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                                                                                                                                                                    diasteromeric excess;
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17; Conser
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100.0%; Pr
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                                                                                                                                                             food additive; drug intermediate; ds; nitrilase;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes an isolated or recombinant polypeptide (I) comprising amino acids having a sequence at least 50 % identical to a sequence (S1) available in electronic form (EC) from the following web site ftp.seqdata.uspto.gov/sequence.html?DocID=2004014195, or its C variants, having one or more mutations at residue 55 Lys, Gly or Glu, at residue 60 glutamic acid, at residue 111 Ser, their combinations or fragments. (I) is useful for: producing an (R)-ethyl 4-cyano-3-thydroxybutyric acid, hydrolysing a nitrile to a carboxylic acid, hydrolysing anyanohydrin moiety or an aminonitrile moiety; producing a chiral alpha-hydroxy acid molecule or a chiral amino acid molecule; producing an (S)-ethyl 4-cyano-3-hydroxybutyric acid, producing an (R)-ethyl 4-cyano-3-hydroxybutyric acid, groducing an (R)-mandelic acid or (S)-mandelic acid, producing (S)-phenyl lactic acid derivative; modifying a molecule; and for identifying a modified compound. The inventive method is useful for monitoring or determining % enantiomerric excess or % diasteromerric excess (I) is useful in the production of food additives and drug continued and continued acid continued and continued acid continued and continued acid continued 
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Best Local
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28-DEC-2000, 2000US-00751299.
21-JUN-2001, 2001US-0300199F.
30-JUL-2001, 2001US-0309006P.
22-JAN-2002, 2002US-031348F.
15-MAY-2002, 2002US-00146772.
09-SEP-2002, 2002US-00241742.
                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ss.
                                                                                                                                                                                                                                     Drosophila melanogaster expressed polynucleotide SEQ ID NO 19922.
                                                                                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                              ABL08480 standard; cDNA; 3530 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 993 BP; 188 A; 330 C; 305 G; 170 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated or recombinant polypeptide having nitrilase activity, useful in production of food additives.
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27-SEP-2001 WO200171042-A2 Drosophila melanogaster

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABS57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                         Streptococcus pneumoniae; type 4 strain
                                                                                                                                                                                                                                                                     Gene; ds; bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                  S. pneumoniae type 4 strain coding region #2428
                                                                                                                                                                                                                                                                                                                                                                 27-OCT-2003
11-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                             ABX08140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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11-JUL-2000;
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 P-PSDB; ABU02847
                                          Masignani V, Tettelin H,
                                                                                                                    27-MAR-2001; 2001GB-00007658
                                                                                                                                               27-MAR-2002; 2002WO-IB002163.
             WPI; 2003-040579/03
                                                                         (GENO-) INST GENOMIC RES.
                                                                                        (CHIR-) CHIRON SPA
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17; Conserv
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2000US-00614150
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(first entry)
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100.0%; Pred. No.
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Sequence 5568 BP; 2066 A; 873 C; 1182 G; 1447 T; 0 U; 0 Other

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cc be amplified, assay comprising contacting a test compound with the compretein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes concoding the proteins has been rendered inactive. The proteins, nucleic encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, cd diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2489 cd identified coding region from the genomic sequence. Note: The sequence data for this patent did not form the part of the printed specification, but was obtained in electronic format directly from WIPO at the fip.wipo.int/pub/published_pct_sequences. (Updated on 27-OCT-2003 to compare the comparence of the 2480 of the protein format directly from wipo at the protein format comparence of the 2480 of the protein format directly from WIPO at the sequence of the 2480 of the protein format directly from wipo at the protein format comparence of the 2480 of the protein format directly from wipo at the protein format comparence of the protein format directly from wipo at the protein format comparence of the protein format directly from wipo at the protein format comparence of the protein format directly from wipo at the protein format comparence of the protein format directly from wipo at the protein format directly from wipo at the protein format comparence of the protein format directly from wipo at the protein format directly from wipo at the protein format directly from wipo at the protein format comparence of the protein format directly from wipo at the protein format directly from wipo at the protein format directly from the protein format directly from 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having the target sequence to substantial complementarity define the termini of the target sequence to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; SEQ ID NO 4855; 56pp; English.
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                                                     30-AUG-2002; 2002US-0407082P
                                                                                                                                            02-SEP-2003; 2003WO-US027401.
                                                                                                                                                                                                                                                                                                                         WO2004020609-A2
                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigenic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S pneumoniae antigenic protein-encoding gene sequence SeqID7
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae infection;
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Best Local Similarity
The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV5254) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52524) are genomic fragments from Streptococcus
                                                                                                                             Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel isolated Streptococcus pneumoniae nucleic acid molecules and the antigenic polypeptides encoded by them. The invention may be useful for the production of compounds with an antibacterial activity or for gene therapy. The nucleic acid molecules, compositions and methods disclosed are useful for treating Streptococcus pneumoniae infection. The present sequence is that of an S pneumoniae gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus pneumoniae nucleic acid molecules, useful for diagnosing, treating and preventing active infections of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
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                                                                                                Claim 1; Page 1085-1094; 1409pp; English
                                                                                                                                                                                            WPI; 1998-272225/24.
                                                                                                                                                                                                                         Dougherty BA;
                                                                                                                                                                                                                                                                                                          31-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae genome fragment SEQ ID NO:171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV52304 standard; DNA; 14736 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 7; 123pp; English.
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                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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Pred. No.
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                                                                                                                               Streptococcus pneumoniae.
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pneumoniae. The present invention also describes an isolated nucleic acid comblecule encoding a homologue of any of the fragments of the S.pneumoniae CR DID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process to the fibrary which contain sequences that comparison to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA. DNA or cDNA produced from an CC organism, amplifying nucleic acid molecules whose nucleic acid molecules corganism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified CC sequences. The computer readable medium can be used in a computer-based commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines
                                                                         for S. pneumoniae
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Query Match Best Local Similarity Seguence 14736 BP; 4665 A; 2568 C; 3255 G; 4247 T; 0 U; 1 Other; 28.8%; Dre 100.0%; Pre 0; Score 17; Pred. No. DB 2; 33; Length 14736;

Ş 42 TGAATCCATCATAAACT 58

Matches 17;

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Mismatches

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밁 13144 TGAATCCATCATAAACT 13128

Job time : 213.485 secs

Search completed: December 22, 2004, 22:44:17

OM nucleic - nucleic search, using sw model

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

December 22,

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Result
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Maximum DB
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US-08-864-357F-10
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US-09-252-991A-3153
US-09-252-991A-353
US-09-252-991A-300
US-09-252-991A-300
US-09-270-767-7800
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                                    Sequence 13572, A
Sequence 4, Appli
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Sequence 16, Appl
Sequence 3113, Ap
Sequence 2863, Ap
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Sequence 3202, Ap
Sequence 1498, Ap
Sequence 7800, Ap
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Sequence 11, Appl
Sequence 17, Appl
Sequence 10, Appl
Sequence 3153, Ap
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Sequence 869, App
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Sequence 7, Appli	Seguence 817, App	Sequence 1, Appl	Sequence 1, Appl:	Sequence 1, Appli	Sequence 3, Appli	Sequence 18, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 35, Appl	-	Sequence 5, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 1, Appli	таду ′от ээлэлбэс

ALIGNMENTS

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RESULT 2
US-08-864-357F-11/c
US-08-864-357F-11/c
Sequence 11, Application US/08864357F
Patent No. 6255281
Use of Recombinant Human Uteroglobin in Treatment of Inflammator
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammator
TITLE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 11612/2
CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
NUMBER OF SEQ ID NO.11
LENGTH: 59
TYPE: DNA
ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: primer sequence
US-08-864-357F-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: primer sequence US-08-864-357F-8
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US-08-864-357F-8
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Best Local Similarity
Matches 59; Conserv
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SEQ ID NO 8
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TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of
TITLE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
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SOFTWARE: PatentIn version 3.0
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TYPE: DNA
ORGANISM: artificial
FEATURE:
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Pred. No. 5.5e-24;
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US-08-961-527-171/c
                                                                    GENERAL INFORMATION:

APPLICANT: Claragen, Inc. & NIH

TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammat.

TITLE OF INVENTION: Fibrotic Conditions
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Best Local
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                                                                                                                                                     Patent No.
FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Charle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PBS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 14736 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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37; Conser
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Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (301) 309-8504
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100.0%; Pred. No. 2.7;
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; OTHER INFORMATION: primer sequence US-08-864-357F-10
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                                                                                                                         Sequence 810, Application US/09252991A

Patent No. 6551795

GENERAL IMPORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR OF SEQ ID NOS: 33142

SEQ ID NO 810

LENGTH: 933

TYDER: NM
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SEQ ID NO 10
LENGTH: 60
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LENGTH: 603
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Best Local Similarity
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Best Local Similarity
                      Query Match
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                      TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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ORGANISM: artificial
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1 Similarity 100.0%; Pred. No. 8.4;
16; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 7.6;
ative 0; Mismatches
27.1%;
100.0%;
  Score 16;
Pred. No.
  DB 4;
8.5;
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RESULT 7
US-09-252-991A-869/c
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US-09-489-039A-1471
                                                                          RESULT 9
US-09-252-991A-3202
                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-1471
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARSUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR TILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 869
LENGTH: 2142
Sequence 3202, Application US/09252991A PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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LENGTH: 309
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPPUTICS
FILE REFERENCE: 2709.2004001
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                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                             237 GCTGAAGAAACTGGT 251
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                                                                                                                                                                                                                                     0; Mismatches
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; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1498
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3202
; LENGTH: 484
; TYPE: DNA
; ORGANIZM: Drosophila melanogaster
US-09-270-767-7800
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US-09-270-767-7800/c
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US-09-489-039A-1498/c
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3002
LENGTH: 342
TYPE: No.
                                                                                                                                                                                                                                             ; Patent No. 6703491 ; GENERAL INFORMATION:
                                                                           APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 7800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATENT NO. 6610836

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION:

PREPRICE:

Z109.2004001

CURRENT APPLICATION NUMBER:

CURRENT FILING DATE:

2000-01-27

PRIOR FILING DATE:

PRIOR FILING DATE:

105-01-29

NUMBER OF SEQ ID NOS:

14342

SEQ ID NO 1498

LENGTH 1360
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CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18
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Query Match

25.4%;

Score 15;

DB 4;

Length 484;

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RESULT 14
US-09-270-767-17063/c
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; ORGANISM: Drosophila melanogaster
US-09-270-767-1781
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US-09-270-767-23082/c
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; ORGANISM: Drosophila melanogaster
US-09-270-767-23082
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1995-03-17
CURRENT FILING DATE: 1995-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1781
LENGTH: 516
TYPE. NN.516
GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION; Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
                                                                                                                                Sequence 17063, Application US/09270767
Patent No. 6703491
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SEQ ID NO 23082
LENGTH: 484
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Patent No. 6703491
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Matches 15; Conser
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ NOS: 62517
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; ORGANISM: Drosophila melanogaster
US-09-270-767-17063
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US-09-489-039A-1476/c
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Job time :
              Search completed: December 23, 2004, 01:33:42
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                                                                                                                                                                                                                                         APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 2709.2004001
CURRENT FLING DATE: 2000-01-27
CURRENT FLING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 1476
LENGTH: 525
TYPE: DN
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1476, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
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SEQ ID NO 17063
LENGTH: 516
TYPE: DNA
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Maximum DB
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                                                                                                                                                                                                                                                          Score
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seq length: 2000000000
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Gapop_60.0 , Gapext 60.0
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59
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/cgn2_6/ptodata/1/pubpna/US07_
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/ Cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/ Cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/ Cgm2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/ Cgm2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/ Cgm2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/ Cgm2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/ Cgm2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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9 US-09-861-688-8

10 US-09-898-616A-3

15 US-10-187-498A-3

16 US-10-647-371-7

9 US-09-861-688-11

10 US-09-881-616A-6

10 US-10-187-498A-6

15 US-10-187-498A-6

16 US-10-647-371-10

17 US-10-437-963-89235

17 US-10-437-963-65306

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              Sequence 8, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 71, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 80, Appli
Sequence 89235, A
Sequence 65306, A
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quenc	equence 34.	equence 581	equence 202	equence 35982,	ce 115741	quence 5306, Ap	equence 112	equence 1420, A	w	equence 5, Appl	Sequence 5, Appl	quence 10. Appl	equence 166	Sequence 171	guence 171,	equence 153	equence 165	quenc	equence 317	equence 317	equence 317	equence 317	equence 72285,	equence 72285	equence 312379.	equence 71225	equence 312379,	equence 71225	equence 51350,	Sequence 51350.	quence 3436, Ap	Sequence 74313, A

ALIGNMENTS

; Sequence 8, Application US/09861688
; Patent No. US20020173460A1
; GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
ITILE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of
ITILE OF INVENTION: Inflammatory and
ITILE OF INVENTION: Inflammatory and
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US/09/861,688
; CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 08/864,357
PRIOR FILING DATE: 2001-05-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8
; LENGTH: 59
TYPE: DNA
; ORGANISM: Artificial Sequence
; PEACURE:
; POTHER INFORMATION: primer sequence
US-09-861-688-8 밁 S US-09-861-688-8 Matches Query Match Best Local (l Similarity 100. 59; Conservative 1 CAGCTGAAGAAACTGGTTGACACCCTGCCGCAGAAACCGCGTGAATCCATCATAAACTG CAGCTGAAGAAACTGGTTGACACCCTGCCGCAGAAACCGCGTGAATCCATCATAAACTG 59 100.0%; Score 59; DB 9; 100.0%; Pred. No. 1.7e-23; Vative 0; Mismatches 0; Length 59 Indels 0 Gaps of. 59 0

RESULT 2 US-09-898-616A-3

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RESULT 3
US-10-187-498A-3
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                                                                                    Matches
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Best Local (
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SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 59
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APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
TITLE OF INVENTION: Imflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00170
CURRENT APPLICATION NUMBER: US/09/898,616A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
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Publication No. US20030109429A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 116142/00260
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Claragen Inc.
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
TITLE OF INVENTION: Inclammatory and Fibrotic Conditions
                                                                                                                                                                                                         NAME/KEY: misc_feature
OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
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OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                             Similarity
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                                                                                 100.0%; Score 59; DB 15; llarity 100.0%; Pred. No. 1.7e-23; Conservative 0; Mismatches 0;
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Publication No. US20040047857A1

GENERAL INFORMATION:

APPLICANT: Claragen, Inc. & NIH

TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory

TITLE OF INVENTION: and fibrotic Conditions

FILE REPERBNCE: 116142-85

CURRENT APPLICATION NUMBER: US/10/647,371

CURRENT PILING DATE: 2003-08-25

PRIOR APPLICATION NUMBER: 09/549,926

PRIOR APPLICATION NUMBER: 09/549,926

PRIOR PRICE SOUTH NUMBER: 09/549,926

PRIOR PRICE SEQ ID NOS: 12

SOUTWARE: Patentin version 3.2

SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of
TITLE OF INVENTION: Inflammatory and
TITLE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 116142/2
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
                                                                                                   Matches
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                                                                                                                      Query Match
Best Local Similarity
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CURRENT FILLMG DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 08/864,357
PRIOR FILING DATE: 1997-05-28
                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                     FEATURE:
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37 CAGCTGAAGAAACTGGTTGACACCCTGCCGCAGAAAC 1
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                                             CAGCTGAAGAAACTGGTTGACACCCTGCCGCAGAAAC 37
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                                                                                                   Conservative
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                                                                                                                      62.7%; Score 37; DB 9; 100.0%; Pred. No. 5.4e-11
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 Mismatches

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; Sequence 6, Application US/09898616A ; Publication No. US20030109429A1 ; GENERAL INFORMATION:

RESULT 6 US-09-898-616A-6/c

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APPLICANT: Claragen Inc.
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
ITILE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of
ITILE OF INVENTION: Inflammatory and Fibrotic Conditions
ITILE OF INVENTION UNDER: US/09/898,616A
CURRENT APPLICATION UNDER: US/09/898,616A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 59
TYPE: DNA
COGRANTSM: Artificial Sequence
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; OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
; OTHER INFORMATION: d sequence maximized for expression in E. coli.
US-09-898-616A-6
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Best Local S
Matches 37
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Publication No. US20030207795A1
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APPLICANT: Pilon, Aprile L
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REPERENCE: 116142/00266
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US 8/864,357
RRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
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                                                        CAGCTGAAGAAACTGGTTGACACCCTGCCGCAGAAAC 1
                                                                                                  CAGCTGAAGAAACTGGTTGACACCCTGCCGCAGAAAC 37
                                                                                                                                                        62.7%; Score 37; DB 15; Length 59; Conservative 0; Mismatches 0; Indels
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Sequence 65306, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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RESULT 10
US-10-437-963-65306/c
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US-10-647-371-10/c
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                                                                                                                                                                                                                                                                                                       APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION UNMERR: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 89235
LENGTH: 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/647,371
CURRENT FILING DATE: 2003-08-25
PRIOR APPLICATION NUMBER: 09/549,926
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 10
LENGTH: 59
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Publication No. US20040047857A1

GENERAL INFORMATION:

APPLICANT: Claragen, Inc. & NIH

TITLE OF INVENTION: dse of Recombinant Human Uteroglobin in Treatment of Inflammatory

TITLE OF INVENTION: and Fibrotic Conditions

FILE REFERENCE: 116142-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                               Matches
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APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Artificial Sequence: primer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                    ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                       FEATURE:
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                                                                           207 AGCTGAÁGAAACTGGTTGÁ 225
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37; Conserv
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Barbazuk, Brad
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                                                                                                                                     32.2%; Err
100.0%; Err
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100.0%; Pr/
                                                                                                                                                              Score 19;
Pred. No.
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Pred. No. 5.4e-11;
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963
                                                                    RESULT 12
US-09-887-576-235/c
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US-10-437-963-65308/c
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US-10-437-963-65306
                Sequence 235, Application US/09887576 Patent No. US20020144047A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 65308
LENGTH: 1152
                                                                                                                                                                                                                          Matches
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APPLICANT: Budworth, P.
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryza sativa
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                                                                                                                                                  668 CTGGTTGACACCCTGCCG 651
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Boukharov, Andrey A.
Barbazuk, Brad
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US-10-437-963-74313
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; ORGANISM: Arabidopsis thaliana
US-09-887-576-235
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                                                                                                                                                                                                                                                      TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221) B (CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 74313 LENGTH: 2134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
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SEQ ID NO 235
LENGTH: 2004
                                                                              Matches
                                                                                                  Query Match
Best Local
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
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APPLICANT:
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TITLE OF INVENTION: Promoters for regulation of
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
CURRENT FILING DATE: 2001-06-25
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                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                 ORGANISM: Oryza sativa
                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                  Local Similarity
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1728 GCTGAAGAAACTGGTTGA 1745
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                                     3 GCTGAAGAAACTGGTTGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou,
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Barbazuk, Brad
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                                                                              Conservative
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                                                                                             30.5%; Score 18; DB 17; Length 2134; 100.0%; Pred. No. 4.1;
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// Sequence 3436, Application US/09974300
// Patent No. US20020146721A1

RESULT 14 US-09-974-300-3436/c

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GENERAL INFORMATION: APPLICANT: Wang, David G.

PAPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Mucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-29
PRIOR PILING DATE: 2000-02-29
PRIOR PILING DATE: 1000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/185,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEC ID NOS: 325720
SEC ID NO 51350
TENGTH: 520
TYPE: DNA
ORGANISM: Human
US-10-027-632-51350
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APPLICANT: Clausen, Ib Groth
ITILE OF INVENTION: Methods For Monitoring Multiple Gene
ITILE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTMARE: FASCSEQ for Windows Version 4.0
SEQ ID NO 3436
LENGTH: 195
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US-10-027-632-51350/c
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; ORGANISM: Bacillus licheniformis
US-09-974-300-3436
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Search completed: December 23, 2004, 05:19:28 Job time: 829.068 secs
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                                                                                                               106 TGAAGAAACTGGTTGAC 90
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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Perfect score:
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ALIGNMENTS

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REFERENCE
AUTHORS
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Pilon,A.L., Mukherjee,A.B. and Zhang,
Use of recombinant human uteroglobin
and fibrotic conditions
Patent: US 6259281-A 9 03-JUL-2001;
Unclassified.
1 (bases 1 to 60)
Pilon,A.L., Mukherjee,A.B. and Zhang,Z.
                                                                                                    Sequence 10 from patent US
AR160919
AR160919.1 GI:16225990
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AR160918
AR160918.1 GI:16225987
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/mol_type="unassigned DNA"
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            AC102189.3 GI:32813512
HTG; HTGS PHAFEI; HTGS DRAFE; HTGS FULLTOP Mus musculus (house mouse)
Mus musculus
                                                                                          AC102189 143233 bp DNA linear H7 Mus musculus clone RP24-216J7, WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of recombinant human uteroglobin in treatment of inflammatory and fibrotic conditions
Patent: US 625281-A 10 03-JUL-2001;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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MacLean, C., Maddonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connox, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schugback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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3 (bases 1 to 143233)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T. Anderson,M., Arachchi,H.M., Camarata,J., Chang,J., Chu Boguslavkiy,L., Boukhgalter,B., Corum,B., De, Chang,J., Ch. Boguslavkiy,L., Chang, C., Corum,B., De, Chang,J., Ch. Boguslavkiy,L., Boukhgalter,B., Corum,B., De, Chang,J., Ch. Boguslavkiy,L., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 16, 2003 this sequence version replaced gi:22381210. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Gide,S., Govd,S., Govette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Largoque,K., College, C., Kamat,A., Karatas,A., Kells,C., Largoque,K., College, C., Kamat,A., Karatas,A., Kells,C., Largoque,K., C., Largoque,K., 
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Birren,B.; Nusbaum,C. and Lander,E.
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Contact: sequence submissions@genome.wi.mit.edu

Center project Information

Center project name: 118187

Center clone name: 216 J 7

Sequenciary sector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 141319 bases at least Q40

Consensus quality: 141319 bases at least Q40
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ORIGIN
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27916. .36443
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20114. .23551
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17767. .20013
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12934. .15356
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mol_type="genomic DNA"

/db_xref="taxon:10090"
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17666 contig of 2210 bp in length
17766 gap of 100 bp
20013 contig of 2247 bp in length
20113 gap of 100 bp
23551 contig of 3438 bp in length
23651 gap of 100 bp
27815 contig of 4164 bp in length
23651 gap of 100 bp
27815 contig of 8528 bp in length
23643; contig of 8528 bp in length
27915 gap of 100 bp
36443; contig of 10224 bp in length
46767; contig of 10224 bp in length
46867; gap of 100 bp
66890; contig of 2023 bp in length
66990; gap of 100 bp
14323; contig of 76243 bp in length
        51.4%;
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Worley, K.C.
Direct Submission
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Best Local Similarity 100. Matches 19; Conservative
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Worley, K.C.
Direct Submission
Submitted (30-UTL-2001) Human Genome Sequencing Center, Depared Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 157842)
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                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                Wu,Y.F., Zhou,J.,
Gibbs,R.
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Homo sapiens 3 BAC RP11-171G7 (Roswell Park Cancer Institute Human
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDMA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 22, 2002 this sequence version replaced gi:20279217. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QUALSTAT-REPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.
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581. .811
/rpt_family="(CA)n"
complement(3582. .3979)
/rpt_family="MSTB"
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complement(1308. .13
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/chromosome="3"
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                                                                                                                                                                    _family="MBR109"
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complement(7020, .722
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_family="L2"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Eng. ZMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMIBE; Information on the WORMIBE database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at the from the library BDT1-11 2 Constructed by the arguments of the database can be found at the from the library BDT1-11 2 Constructed by the Group can be found at the from the library BDT1-11 2 Constructed by the Group can be found at the from the library BDT1-11 2 Constructed by the Group can be found at the from the library BDT1-11 2 Constructed by the Group can be found at the from the library BDT1-11 2 Constructed by the Group can be found at the group can be group can be group can be group c
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Submitted (21-JAN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 21, 2003 this sequence version replaced gi:27803162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RP11-558F24 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Loses 1 to 163934)
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Human DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
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   CAGTCTAGCCTGTGCAAC 44926
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                       /clone="RP11-558F24"
/clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo gapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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100.0%;
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APPO1303

REPO1303

ROWSHOES, 26 unordered pieces.

ROWAPO1903.2 GI:8117554

APO1303.2 GI:8117554

APO1303.2 GI:8117554

NAPO1303.2 GI:8117554

APO1303.2 GI:8117554

HOMO sapiens

Eukaryota; Metacaca; Chordata; Craniata; Vertebrata; Euteleostomi; Memo sapiens (human)

NES HOMO sapiens

Eukaryota; Metacaca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo:

NES 1 to 167082)

RE 1 to 167082; Primates; Catarrhini; Hominidae; Homo:

NES 1 to 167082)

NED 2 (bases 1 to 167082)

NED 3 to 167082; Novoda, A., Taylor, T.D., Hong-Seog, P., Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. Enstitute of Physical Research (ERIEM)

Shifett Submisted

Opposited (Physical Research (ERIEM)

Shomitted (24-pR-2000) Masahira Hattori, The Institute of Physical Research (ERIEM)

Submitted (24-pR-2000) Masahira Hattori, The Institute of Physical Research (Physical Research (ERIEM)

Submitted (24-pR-2000) Masahira Hattori, The Institute of Physical Research (Physical Research (Ph
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NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1 22433 contig of 22434 bp in length
45118 59868 contig of 14751 bp in length
59969 71793 contig of 11825 bp in length
71894 81974 contig of 11825 bp in length

149631 153039 108765 113727 138480 142988 104814 146648 129966 22534 45118 59969 71894 20207 108664 104713 149530 146547 contig contig contig contig conti cont conti conti contig conti conti in length
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160378 162841 contig of 2464 bp in length
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16498 166310 contig of 1613 bp in length
164411 167082 contig of 672 bp in length
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/db_xref="taxon:9606"
/chromosome="18"
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152938: contig of 3308 bp in length
153038: gap of 100 bp
155111: contig of 2073 bp in length
155211: gap of 100 bp
157376: contig of 2165 bp in length
157476: gap of 100 bp
160277: contig of 2801 bp in length
160377: gap of 100 bp
162841: contig of 2464 bp in length
162941: gap of 100 bp
162941: contig of 1656 bp in length
164597: contig of 1656 bp in length
164597: gap of 100 bp
164670: gap of 100 bp
166410: contig of 1653 bp in length
166410: gap of 100 bp
166710: contig of 672 bp in length
167082: contig of 672 bp in length
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71793: contig of 11825 bp in length
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4: contig of 3851 bp in length
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5: contig of 3361 bp in length

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9: contig of 4953 bp in length
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contig of 6893 bp in length
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contig of 6180 bp in length
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contig of 3560 bp in length
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contig of 9366 bp in length
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.66411. .167082
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64698. .166310
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60378. .162841
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42988. .146547
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08765. .113626
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AUTHORS
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AC102275
   REFERENCE
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ORGANISM
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                                                              Mus musculus, clone RP24-290E7
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 169230)
Birren,B., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                             Mus musculus
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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AC102275.2
                               Unpublished
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   (bases 1 to 169230)
                                                                                                                                                                                                                                                         musculus (house mouse)
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/evidence=not_experimental
/rpt_family="L1M4"
25717...26058
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/rpt_family="AluSx"
27982. .28268
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/rpt_family="AluSx"
27486, ,27783
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/evidence=not_experimental
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complement(23261. .23563)
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/rpt_family="AluJb"
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/rpt_family="L1ME1"
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/rpt_family="AluSq"
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'rpt_family="Aluy"
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'rpt_family="AluJb"
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/rpt_family="AluJo"
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100.0%; Pred. No. 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RS Birren, B.; Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhqalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Colling, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitchligh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Laroque, K., Linders, C., Kamat, A., Kells, C., Laroque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., McCarthy, M., McDwan, P., McKernan, K., McPheteter, R., Meldrim, J., McCarthy, M., McDwan, P., McKernan, K., McPheteter, R., Meldrim, J., McCarthy, M., McDwan, P., McKernan, K., McPheteter, R., Meldrim, J., Morbu, C., Wilova, T., Mlenga, V., Murpby, T., Naylor, J., Wguyen, C., Norbu, C., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Oliver, J., Feterson, K., Phunkhang, P., Pierre, N., Pollara, V., Roman, J., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stopanovic, N., Stansson, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Ville, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zalnoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-APR 2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On Apr 17, 2003 this sequence version replaced gi:17061361. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                be preserved.
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   121665
121765
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121664: contig of 121664 bp in length 121764: gap of 100 bp 122426: contig of 662 bp in length
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155547
156698
156798
158479
1588579
158579
159754
159854
161009
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129774: contrig of 869 bp in length
129874: gap of 100 bp
131603: contrig of 682 bp in length
131603: contrig of 947 bp in length
131703: gap of 100 bp
1313498: contrig of 103 bp in length
134340: contrig of 681 bp in length
134340: contrig of 681 bp in length
13539: contrig of 683 bp in length
135439: gap of 100 bp
135439: gap of 100 bp
137116: contrig of 774 bp in length
136402: gap of 100 bp
137216: gap of 100 bp
137316: gap of 100 bp
137317 gap of 100 bp
137318 gap of 100 bp
137319 gap of 100 bp
137319 gap of 100 bp
144736: contrig of 779 bp in length
143956: gap of 100 bp
144736: contrig of 779 bp in length
14436: gap of 100 bp
14436: gap of 100 bp
14436: gap of 100 bp
144736: contrig of 679 bp in length
14436: gap of 100 bp
144736: contrig of 679 bp in length
144736: contrig of 132 bp in length
144736: contrig of 132 bp in length
144736: gap of 100 bp
144736: contrig of 132 bp in length
144736: gap of 100 bp
145268: gap of 100 bp
146268: gap of 100 bp
146368: gap of 100
15546: contig of 1544 bp in length
15646: gap of 105 bp
156697: contig of 1051 bp in length
156797: gap of 100 bp
158478: contig of 100 bp
15973: contig of 100 bp
159753: gap of 100 bp
16108: contig of 1175 bp in length
161108: gap of 100 bp
161235: contig of 1127 bp in length
162335: gap of 100 bp
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/note="assembly_fragment"
131704. .132737
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68287 74443 contig of 6659 bp in length
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URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
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Center project Information
Center project name: HumDraft18
Center clone name: RP11-819X4

Center clone name: RP11-819X4

Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 152541 bases at least Q40
Consensus quality: 152541 bases at least Q30
Consensus quality: 167578 bases at least Q30
Insert size: 170121; sum-of-contigs
                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                              as soon as it is available and be preserved.
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22518: contig of 22518 bp in length 22618: gap of 100 bp 36257: contig of 13639 bp in length 36357: gap of 100 bp 47612: contig of 11255 bp in length 47712: gap of 100 bp 57975: contig of 10263 bp in length 58075: gap of 100 bp
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72921: contig of 315
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g of 3516 bp
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC091843 linear PRI 27-FEB-
Homo sapiens chromosome 5 clone CTD-2185023, complete sequence.
                                                                        Direct Submission
Submitted (27-FEB-2002) DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 27, 2002 this sequence version replaced gi:15290412.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                 Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US 1 (bases 1 to 177056)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 17705)

DOE Joint Genome Institute and Stanford Human Genome Center.
                    Finishing Completed at Stanford Human Genome Center
Quality: Phrap Quality >=40 100% of Sequence,
                                                        www.jgi.doe.gov
                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                             2 (bases 1 to 177056)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment" 161866. .164392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
107386. .113439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
95449. .101895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
158964. .161765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
155826. .158863
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151516. .155725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
140679. .144357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148074. .15141
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144458. .147973
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132130. .136178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
113540. .120229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88367. .95348
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148074. .151415
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DEFINITION ACCESSION
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AC090210/c
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TITLE
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CE 2 (bases 1 to 180851)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A.,

Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Collymore, A., Cooke, P., DeArellano, K., Gaspe, D., Galagan, J.,

Bargayna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gard-Pierre, N.,

Hagos, B., Heaford, A., Horton, L., Halmew, I. 11ev, I., Johnson, R.,

Jones C., Karatas, A., Larocque, K., Lamazares, R., Landers, T.,

Lehoczky, J., Ievine, R., Liu, G., MacLean, C., Macdonald, P.,

Marquis, N., Matthews, C., McCarthy, M., McDwan, F., McKernan, K.,

McPheeters, R., Melldrim, J., Meneus, L., Mihova, T., Mlenga, V.,

Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,

O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,

Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,

Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,

Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,

Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,

Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A.,

Wilson, B., Wi, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,

Rojenbek, L., Zimmer, A. and Zody, M.
E 3 (bases 1 to 180951)

28 Sirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, C., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, C., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacCarthy, M., McEwan, P., Major, J., Marquis, N., Matthews, C., MecCarthy, M., McEwan, P., Major, J., Murphy, T., Naylor, J., Nguyen, C., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
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Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-720N18
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/chromosome="5"
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100.0%; Pred. No.
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                            TITLE
JOURNAL
                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 26, 2001 this sequence version replaced gi:14192981. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
Mammalia; Eutheria; Primates; Catarrhini; Hominid (bases 1 to 181211)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hom Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Homo sapiens 181,211 genomic DNA of 18q21
Published Only in DataBase (2000)
2 (bases 1 to 181211)
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 18 clone RP11-720N18 map 18q21, WCRKING DRAFT SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                    AP001904.2 GI:8117555
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 180851: contig of 180851 bp in length.
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/clone_lib="RPCI-11 Human Male BAC"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        175328 178652 contig of 3325 bp in length
178753 181211 contig of 2459 bp in length
Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently
consists of 15 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preserved
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Center project name: HumDraft18
Center clone name: RP11-720N18
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Contact: hattori@gsc.riken.go.jp
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33400: gap of 100 bp
54981: contig of 21581 bp in length
55081: gap of 100 bp
73468: contig of 18387 bp in length
73568: gap of 100 bp
94430: contig of 20862 bp in length
94530: gap of 100 bp
113614: contig of 19084 bp in length
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AC136510.17 GI:45544719
HTG; HTGS_PHASE2; HTGS_DRAFT
Pan troglodytes (chimpanzee)
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Pan troglodytes clone pieces.
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36383 CAGTCTAGCCTGTGCAAC 36400
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* by the finished sequence as soon as it is available and

* the accession number will be preserved.

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                                                     16 CAGTCTAGCCTGTGCAAC 33
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3 (bases 1 to 186110)
Lau, C. C.Y. and Roe, B.A.
Direct Submission
Submitted (18-MAR-2004) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, Or 700 Parrington Oval, Room 208, Norman,
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Center: Department Of Chemistry And Biochemistry
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On Mar 18, 2004 this sequence version replaced gi:45476613
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Lau, C.C.Y. and Roe, B.A.
Direct Submission
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Lau, C.C.Y. and Roe, B.A.
Pan troglodytes BAC Clone rp43-27h3
Unpublished
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                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/mol type="genomic DNA"
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Add14/83 Hullain SIC Ade56935 Rat gene		Human	Humar	Aaa28522 Human opi	Aaa28526 Human opi	Add44906 Rat gene	Aaa28524 Human opi	Aax37460 Human sec	Aaz24882 Human sec	Add35086 Mouse mit	Aai92367 Human pol	Ach14100 Human adu	Aak69660 Human imm	Aak69659 Human imm	Aak69658 Human imm	Adl27630 Recombina	Abz58374 Human ute	Adl27629 Recombina	Abz58373 Human ute	Description

The present sequence is that of oligonucleotide 4, which was used in the construction of a synthetic gene for the production of human uteroglobin (hUG) in bacteria. Oligonucleotides 1-4 (see ABZ58370-73) were used to assemble the coding strand and oligonucleotides 5-8 (see ABZ58374-77) the complementary strand. The gene was assembled by annealing and ligation of the oligonucleotides. Because mature native hUG has glutamic acid at its N-terminus, an initiator methionine was added to the N-terminus, and

Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic gene which codes for human uteroglobin.

Claim 1; Page 33; 127pp; English.

WPI; 2003-221527/21.

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Adb96941 Human MDR	Adb87958 Human UGT	Adb20869 MRP1 base	Acf62750 Cancer ba	Adb92114 Human MDR	Adb96923 Human MDR	Adb87940 Human UGT	Adb20851 MRP1 base	Acf62736 Cancer ba	17382 Human	Abq77404 Human SEL	Adm93170 Human KOX	Adm93169 Human KOX	Adi36730 Genomic D	Adi36729 Genomic D	Aas23002 DNA encod	Aas22908 DNA encod	Aai63476 Human kid	Aak67907 Human imm	Aak81002 Human imm	Aai99126 Human exc	-	Aadl6913 Human pho	Adal5021 Murine an

ALIGNMENTS

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The invention relates to a bacterial expression system for the production of recombinant human uteroglobin (rMU), comprising a synthetic gene or human cDNA sequence which codes for human UG, constructed from the oligonucleotides appearing as ADL27626-ADL27629, and which further comprises Met-Ala At the N-terminus of the sequence. Also included are producing an rMUG master cell bank (comprising inoculating a suitable incubating broth with an aliquot portion of a rMUG research seed bank to form a bacterial culture, incubating the bacterial culture, adding a cryopreservative to the bacterial culture to form a cryopreserved solution, transferring a portion of the cryopreserved solution to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention, the synthetic gene was cloned into plasmid pCG12 [see ABZ58378] and recombinant hUG (see ABF72259) was produced in Escherichia coli strain CG12. The invention relates generally to the production of recombinant hUG by bacterial expression, protein purification and scaled up production according to current good manufacturing practices. The recombinant hUG is useful for the treatment of inflammatory and fibrotic conditions, such as meonatal respiratory distress syndrome and bronchopulmonary dysplasia. It may also be used to treat conditions associated with elevated phospholipase A2 levels such as pancreatitis,
                                                                                                                                                                                                                                                        Bacterial expression system for production of recombinant human uteroglobin comprising synthetic gene or human cDNA sequence who for human uteroglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ss; recombinant human uteroglobin; rhUG; bacterial expression system; rhUG master cell bank; rhUG research seed bank; anti-inflammatory; secretory phospholipase A 2; fibronectin; respiratory distress; inflammation; fibrotic disease.
                                                                                                                                                                                                                                                                                                                                         WPI; 2004-051527/05
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02-JUL-2001; 2001US-00898616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acute renal failure, rheumatoid arthritis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon usage was optimised for expression in bacteria. In an example from
                                                                                                                                                                                                                    Claim 1; SEQ ID NO 4; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     (PILO/) PILON A L. (WELC/) WELCH R W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 37
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                                                                                                                                                                                                                                                                                                                                                                                 Welch RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human uteroglobin, rhUG, coding oligonucleotide
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Pred. No.
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cryovial and storing the cryovial at a temperature below -60 degrees C), expressing rhUG (comprising providing a production seed cell bank culture comprising an expression vector capable of expressing rhUG, inoculating a broth medium with the production seed cell bank culture to form an cinculating a large scale fermenter with the inoculum formed from the step (c) to form a fermentation culture formed in step (b), culture within the large scale fermenter, adding an induction agent to culture within the large scale fermenter, adding an induction agent to the fermentation culture to induce the expression of rhUG and harvesting the above fermentation culture), purifying rhUG, determining the potency of rhUG in a sample, measuring in vitro anti-inflammatory effect arising from inhibition or blocking of secretory phospholipase A 2 enzymes by rhUG, measuring in vitro binding of rhUG to fibronnectin, determining the purity of rhUG, and a pharmaceutical composition comprising a purified rhUG and a carrier or diluent. The bacterial expression system is useful for producing a rhUG research seed bank or a pharmaceutical grade rhUG diseases. The rhUG is useful for treating inflammation and fibrotic constraint the surchaft churcher; thus compared to a parifical cused to
                                                         the synthetic rhUG gene.
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Matches
                                                         Query Match
Best Local
                                                                                               Sequence 37 BP; 11 A; 8 C; 10 G; 8 T; 0 U; 0 Other;
                                               37;
                                                            Similarity
ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG
                     ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 37
                                               Conservative
                                                          100.0%;
                                                                     100.0%;
                                               o
\.
                                                          Score 37;
Pred. No.
                                               Mismatches
                                                         4.8e-11;
                                                                        DB 12;
37
                                                                       Length 37
                                                 Indels
                                               ٥,
                                               Gaps
                                               0,
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밁 Ś

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RESULT 3
                                                                                 Human uteroglobin synthetic gene oligonucleotide
                                                                                      28-APR-2003
                                                                                           ABZ58374;
                                                                                                ABZ58374
                                                                                                standard; DNA; 60
                                                                                      (first entry)
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Human; uteroglobin; respiratory distress; antiinflammatory; antifibrotic; antiinflammatory; antiasthmatic; nephrotropic; antirheumatic; antiarthritic; ss.

sapiens

WO2003003979-A2

16-JAN-2003

02-JUL-2002; 2002WO-US020836.

02-JUL-2001; 2001US-00898616.

(CLAR-) CLARAGEN INC

Pilon AL, Welch RE;

WPI; 2003-221527/21.

Bacterial expression system for producing recombinant human uteroglobin for treating inflammatory and fibrotic conditions, comprises a synthetic gene which codes for human uteroglobin.

Example 1; Page 33; 127pp; English

The present sequence is that of oligonucleotide 5, which was used in the construction of a synthetic gene for the production of human uteroglobin (hUg) in bacteria. Oligonucleotides 1-4 (see ABZ58370-73) were used to assemble the coding strand and oligonucleotides 5-8 (see ABZ58374-77) the

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RESULT 4
ADL27630/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention, the synthetic gene was cloned into plasmid pCG12 (see ABZ58378) and recombinant hug (see ABP72259) was produced in Escherichia coli strain CG12. The invention relates generally to the production of recombinant hug by bacterial expression, protein purification and scaled up production according to current good manufacturing practices. The recombinant hug is useful for the treatment of inflammatory and fibrotic conditions, such as neonatal respiratory distress syndrome and bronchopulmonary dysplasia. It may also be used to treat conditions associated with elevated phospholipase A2 levels such as pancreatitis, associated with elevated phospholipase A2 levels such as pancreatitis,
                                                                                                                                                                                                                                                                                                                                                  28-MAY-1997; 97US-00864357.
02-JUL-2001; 2001US-00898616.
                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2002; 2002US-00187498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; recombinant human uteroglobin; rhUG; bank; bacterial expression system; rhUG master cell bank; bacterial expression system; rhUG master cell bank; bacterial expression system; rhUG master y secretory phospholipase A fibronectin; respiratory distress; inflammation; fibrotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL27630 standard; DNA; 60 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 60 BP; 13 A; 14 C; 15 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-terminus, an initiator methionine was added to the N-terminus, a codon usage was optimised for expression in bacteria. In an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complementary strand. The gene was assembled by annealing and ligation the oligonucleotides. Because mature native hUG has glutamic acid at it
                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003207795-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant human uteroglobin, rhUG, non-coding oligonucleotide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acute renal failure, rheumatoid arthritis and asthma
                                                                                                                                                             uteroglobin comprising synthetic for human uteroglobin.
                                                                                                                                                                                                                                   WPI; 2004-051527/05.
                                                                                                                                                                                                                                                                Pilon AL,
                                                                                                                                                                                               Bacterial expression system for production of recombinant human
                                                                                                                                                                                                                                                                                                   (WELC/) WELCH R W.
                                                                                                                                                                                                                                                                                                                       (PILO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 1
                                                                                                                                                                                                                                                                  welch RW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Pred. No. 4.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                             gene
                                                                                                                                                                               or human cDNA sequence which codes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    its
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The invention relates to a bacterial expression system for the production of recombinant human uteroglobin (rhUg), comprising a synthetic gene or human cDNA sequence which codes for human UG, constructed from the oligonucleotides appearing as ADL27626-ADL27629, and which further comprises Met-Ala-Ala at the N-terminus of the sequence. Also included are producing an rhUG master cell bank (comprising inoculating a suitable incubating broth with an aliquot portion of a rhUG research seed bank to

Example 1; SEQ ID NO 5; 64pp; English.

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RESULT 5
AAK69658/c
ID AAK696
XX AAK696
XX AAK696
XX Human;
KW Cytost
XX Homo s
XX Hom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC cryopreservative to the bacterial culture to form a cryopreserved consistent transferring a portion of the cryopreserved solution to a cryopresid and storing the cryovial at a temperature below -60 degrees C). CC expressing rhUG (comprising providing a production seed cell bank culture C comprising an expression vector capable of expressing rhUG, inoculating a broth medium with the production seed cell bank culture c inoculum, incubating the bacterial culture formed in step (b). CC inoculum, incubating the bacterial culture formed in step (b) form an cc inoculating a large scale fermenter with the inoculum formed from the step (c) to form affermentation culture, incubating an induction agent to culture within the large scale fermenter, adding an induction agent to the fermentation culture; purifying rhUG, determining the potency of rhUG in a sample, measuring in vitro anti-inflammatory effect arising CC the fermentation or blocking of secretory phospholipase A 2 enzymes by cryUG, measuring in vitro binding of rhUG to fibronectin, determining the curity of rhUG, and a pharmaceutical composition comprising a purified cry producing a rhUG research seed bank or a pharmaceutical grade rhUG distress. The rhUG is useful for treating inflammation and fibrotic diseases. The present sequence is a non-coding strand oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                          07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
                                                                                                                                                30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                         19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; gene therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK69658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK69658 standard; DNA; 698 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60 BP; 13 A; 14 C; 15 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used to construct the synthetic rhUG gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2001; 2001WO-US001354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24470:
                                                                                                                                                                                                                                                                                                                                     17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                    2000US-0209467P.
2000US-0214886P.
2000US-0215135P.
2000US-0216647P.
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                             2000US-0217487P.
2000US-0217496P.
2000US-0218290P.
                                                                                                                                                                                                                                                                                                        2000US-0190076P.
2000US-0198123P.
                                                                                                                                                                                                                                                                          2000US-0205515P
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8e-11;
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2000US-0235336P

2000US-0235336P

2000US-023636P

2000US-023636P

2000US-023636P

2000US-023636P

2000US-023636P

2000US-0236370P

2000US-023680P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0241809P

2000US-0241809P

2000US-0241809P

2000US-0241809P

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2000US-0241809P

2000US-0241809P
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2000US-0232398P
2000US-0232399P
2000US-0232400P
2000US-0232401P
2000US-0233063P
2000US-0233065P
2000US-0234223P
2000US-0234223P
2000US-0234223P
2000US-0234299P
2000US-023499P
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2000US-0229287P.
2000US-0229343P.
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2000US-0232081P.
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        CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cartivity, and can be used in gene therapy and vaccine production. (I) CC arctivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polymuleotides may be used to produce the secreted (I), by inserting the culeic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polymucleotides may be used to produce the segment. (CC diagnose and treat immune/haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic derived cells. AAK64703 CC to AAK87694 represent human immune/haematopoietic antigen genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 24470; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                           WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                        Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L7-NOV-2000
                                                                                                                                                                                                                                                                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000US-0246476P.
; 2000US-0246477P.
; 2000US-0246478P.
                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-0259678P
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2000US-0246610P
2000US-0246611P
                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
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08-SEP-2000;

06-SEP-2000; 08-SEP-2000; 08-SEP-2000;

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RESULT 6
AAX69659/
AAX69659;
XX
AC AAX69659;
XX
AC AAX69659;
XX
DE Human immune/haematopoietic antig
XX
Human immune/haematopoietic; im
XX
Cytostatic; gene therapy; vaccine
XX
PM WC200157182-A2.
XX
C9-AUG-2001; 2001WO-US001354.
XX
PM Human; immune/haematopoietic; im
XX
PM WC200157182-A2.
XX
C9-AUG-2001; 2001WO-US001354.
XX
PM Human; immune/haematopoietic; im
XX
PM WC200157182-A2.
XX
C9-AUG-2001; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 11-JAN-2000; 2000US-0180628P.
PR 11-JAN-2000; 2000US-0180555.P.
PR 11-MAR-2000; 2000US-0180530P.
PR 11-MAR-2000; 2000US-018133P.
PR 11-JUL-2000; 2000US-018133P.
PR 11-JUL-2000; 2000US-018133P.
PR 11-JUL-2000; 2000US-0216647P.
PR 11-JUL-2000; 2000US-0216839P.
PR 11-JUL-2000; 2000US-021684P.
PR 11-JUL-2000; 2000US-021684P.
PR 11-JUL-2000; 2000US-021684P.
PR 11-JUL-2000; 2000US-021684P.
PR 11-JUL-2000; 2000US-0217496P.
PR 11-JUL-2000; 2000US-0218299P.
PR 11-JUL-2000; 2000US-0225213P.
PR 11-JUL-2000; 2000US-0225214P.
PR 11-JUL-2000; 2000US-0225279P.
PR 11-JUL-2000; 200
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 698 BP; 270 A; 116 C; 107 G; 205 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AGTCTAGCCTGTGCAA 32
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664 AGTCTAGCCTGTGCAA 649
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14-SEP-2000;
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2000US-0233065P.
2000US-0234223P.
2000US-0234274P.
2000US-023497P.
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2000US-0232401P.
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2000US-0237037P
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RESULT 7
AAK69660/c
                                                                                                                                                                                                                                                           CC antino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cantivity, and can be used in gene therapy and vaccine production. (I) creatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome cathet the patients of production of (I) by expression for complete the patients own production of (I). Additionally, (I) concluded the patients own production of (I). Additionally, (I) conclude acids into a host cell and culturing the cell to express the proteins and polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the concers and cancer metastases of haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAX54920 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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Best Local :
                                                                                                                                                                                 Matches
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06-DEC-2000;
08-DEC-2000;
06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                           AAK69660;
                                                     AAK69660 standard; DNA; 699
                                                                                                                                                                                                                                      Sequence 699 BP; 270 A; 116 C; 107 G; 206 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 24471; 3071pp + Sequence Listing; English.
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17-NOV-2000;
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16; Conserv
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2000US-0251988P
2000US-0256719P
2000US-0251479P
2000US-0251858P
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2000US-0251869P
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2000US-0249215P
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2000US-024921P
2000US-0249244P
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2000US-0254097P.
2001US-0259678P.
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7 100.0%; F1
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112-SEP-2000
114-SEP-2000
114-SEP-2000
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01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
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227182P.
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2000US-0234273P.
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2000US-023499P.
2000US-0235484P.
2000US-0235834P.
  RESULT 8
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ID ACH1
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Matches
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                        (DRMA/)
(LABA/)
(STAC/)
(DICK/)
                                                                                                                                                                                                                                                                                                                                                                                                            Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human adult brain cDNA #1312.
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08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
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STACHE-CRAIN B.
DICKSON M C.
JONES L W.
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RESULT 9
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated CDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030073623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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WPI; 2001-514838/56
P-PSDB; AAC12436.
                                                                                     Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine;
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18-MAY-2000; 2000US-00577409
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                                                                                                                                                   (HYSE-) HYSEQ INC.
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                                                                                         Liu C,
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                                                                                                                                                                                                                                                       2000US-00515126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell proliferation; cell differentiation; gene therapy;
                                                                                            Drmanac
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 621 BP; 152 A; 162 C; 137 G; 168 T; 0 U; 2 Other;
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31-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
mitochondrial disease; oxidative phosphorylation dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse mitochondrial DNA sequence SEQ ID NO:2866.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Wallace DC,
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2001CA-02356540
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100.0%; Pred. No.
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The invention relates to a novel array comprising at least two isolated nucleotide molecules, each molecule having a sequence capable of uniquely hybridising to a nucleic acid molecule which is an expression product of a gene involved in mitochondrial biology. The array comprises two or more isolated nucleic acid molecules or spots, each molecule having a sequence

Array containing probes for genes involved in mitochondrial biology, useful for determining mitochondrial biology gene expression profiles for use in diagnosing pathologies and identifying biochemical pathways.

Claim 2;

SEQ ID NO 2866; 201pp; English.

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Condition of the probes of the in
19-MAR-1998;
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19-MAR-1998;
                                                                                                                                                                                                                                                                                               Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restencesis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditts; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein gene 72 clone HE6GA29.
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                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                18-MAR-1999;
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                    98US-0078563P.
98US-0078566P.
98US-0078573P.
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01-APR-1998;
01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAZ24902) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ24811-Z24907; amino acid sequences AAX41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides in a sample or determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 95 polynucleotides, based on which tissues they are most highly expressed in the new polynucleotides. Specific uses are described for each of the
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19-MAR-1998;
19-MAR-1998;
                                                                                                                                                        Human; secreted protein; treatment; prevention; protein therapy; AIDS; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; fetal deficiency; blood disorder; luckemia; immune system disease; autoimmune disease; hepatic disease; lymphoma; renal disease; inflammation; allergy; Alzheimer's disease; schizophrenia; cognitive disease; prostate disease; skeletal; cardiac; muscle disorder; publicate disease; skel
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                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein cDNA fragment containing gene 10
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                                                                                                                                arthritis; malignancy; digestive; endocrine; infection;
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98US-0080313P
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חיים RD,
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H, Ebner R,
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1.1e+
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R, Lafleur DW,
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Olsen HS;
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Homo sapiens.

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RESULT 13
AAA28524
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                                                                                                                                                                                                                                                                                                                                           CC This invention describes novel isolated human genes and the secreted CC proteins they encode. The products of the invention are useful for CC preventing, treating or ameliorating medical conditions, e.g. by protein CC or gene therapy. Also pathological conditions can be diagnosed by CC determining the amount of the new polypotides in a sample or by CC generating the presence of mutations in the new polypotides. CC specific uses are described for each of the 101 polynucleotides, based on CC which tissues they are most highly expressed in, and include developing CC products for the diagnosis or treatment of cancer, tumours, CC neurodegenerative disorders, leukemias, diseases of the immune system, CC deficiencies, bepatic and renal diseases, lymphomas, inflammation, CC allergies, Alzheimer's and cognitive disorders, schizophrenia, prostate CC disease, skeleral or cardiac muscle disorders, pulmonary disorders, CC transplant rejection, disorders involving osteoclasts such as CC infections and AIDS. The human secreted proteins of the invention are represented in AAY07451-X37552
                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                  Matches.
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Ferrie AM,
            OGFr; opioid growth factor receptor; growth inhibitor; proliferative; cytostatic; vulnerary, gene therapy; antagonist; chromosome 20q13.3; ss.
                                                    Human opioid growth factor receptor cDNA spliced version
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                                                                                 29-AUG-2000
                                                                                                                                       AAA28524 standard; cDNA; 1601
                                                                                                                                                                                                                                                                                                                      Sequence 1089 BP; 367 A; 202 C; 240 G; 279 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isclated human genes and the secreted polypeptides they encode.
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                                                                                                                                                                                                                                                                            Similarity
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97US-0060843P.
97US-0060862P.
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97US-0060880P.
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ų σ,
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A, Feng P;
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RESULT 14
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ID ADD449
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                 Rat; ds; gene; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                              ADD44906;
                                                                                                                                                                                                                                                            ADD44906 standard; DNA; 1756 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cDNA encoding rat and human opioid growth factor receptors which modulate cell growth, useful for treating cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PENN-) PENN STATE RES FOUND
                                                                                                                gene Y15054, SEQ ID NO 10337
                                                                                                                                                                                                                                                                                                                                                                               1253 TGGAGAAGATCGCTC 1267
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DB; AAY92810.
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34. .1419
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420. 1601
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100.0%; Pred. No. 1.1e+C
ltive 0; Mismatches
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RESULT 15
AAA28526
ID AAA28
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AC AAA28
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DT 29-AU
XX
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Best Local S
Matches 15
                    29-AUG-2000
                                                         AAA28526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page; 1017pp;
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(FARB )
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                    (first
                                                                                                                                                                                                                                                                                                                                              355 A; 543 C; 484 G; 374 T; 0 U; 0 Other;
                                                                                            CDNA; 2289
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Pred. No. 1.1e+02;
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                                                                                                                                           CC Primers generated from rat opioid growth factor receptor (OGFr) cDNA were closed to clone a fragment of the human OGFr cDNA. The complete sequence of human OGFr was assembled with a combination of 3 and 5 RACE FC consistently yielded a single species of cDNA, while the 3 RACE revealed extensive alternative splicing. The alternate splice forms were missing the imperfect repeats or differed in the number of imperfect repeats. The location was determined by FISH as 2013.3. CC OGFr proteins, nucleic acid molecules, antibodies, transformed cells and CC expression vector are useful for detecting expression or levels of an CC OGFr in a tissue. OGFr nucleic acids can be used to inhibit growth of cells in vitro. The antisense sequences and antibodies can be used to promote growth of cells in vitro. Cell growth can be promoted by components of the OGF ligand-receptor system, especially where a cc subject suffers from a tissue wound. Treating cancer comprises enhancing the function of the OGF ligand-receptor system in cancerous cells of a patient or administering the OGFr nucleic acid to the patient
                                                              Matches
                                                                           Query Match
Best Local
                                                                                                                     Sequence 2289 BP; 470 A; 714 C; 809 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cDNA encoding rat and human opioid growth factor receptors which modulate cell growth, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 87-89; 91pp; English.
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 1253
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                            2 TGGAGAAGATCGCTC 16
                                                                             Similarity
TGGAGAAGATCGCTC
                                                            Conservative
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34. .2007
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/product= "Opioid_growth_factor_receptor"
2008. .2289
/*tag= c
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                                                                           100.0%;
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                                                                           Score 15;
Pred. No.
                                                          Mismatches
                                                                                                                     296 T; 0 U; 0 Other;
                                                         DB 3; Le
1.1e+02;
hes 0;
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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seq length: 2000000000
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37
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       100.
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| Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Compage | Com
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US-08-664-357F-10

US-09-234-245-1

US-08-760-534A-5

US-09-336-757-5

US-09-336-757-5

US-09-621-976-12461

US-08-463-115-26
US-09-252-991A-5999

US-08-463-115-2

US-08-465-388-2

US-08-475-388-2

US-09-252-991A-6306

US-09-99-411-298

US-08-472-217-3

US-08-760-534A-3

US-09-566-877-131

US-09-566-877-131

US-09-568-877-183

US-09-586-877-183

US-09-580-412C-183

US-09-98-419-183

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US-09-98-049-18
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US-08-463-115-18
US-08-465-388-18
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Sequence 5999, Ap
Sequence 2, Ar-
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Sequence 10, Appl
Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 3565, Appli
Sequence 12461, A
Sequence 26, Appl
Sequence 26, Appl
Sequence 18, Appl
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Sequence 2, Appli
Sequence 6306, Ap
Sequence 298, App
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  3, Appli
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423	410	369	348	348	342	301	301	297	289	289	271	4411529	4403765	1830121	1830121	1830121	72604
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US-09-252-991A-11388	US-09-221-017B-273	US-09-270-767-14734	US-09-431-202-3	US-08-844-059-3	US-10-101-464A-147	US-09-270-767-17395	US-09-270-767-2113	US-09-252-991A-8030	US-09-194-036B-12	US-08-651-155B-12	US-09-313-294A-695	US-09-103-840A-1	US-09-103-840A-2	US-10-329-960-1	US-09-643-990A-1	US-09-557-884-1	US-09-65/-4/4-/
Sequence 11388, A	Sequence 273, App	Sequence 14734, A	Sequence 3, Appli	Sequence 3, Appli	Sequence 147, App	Sequence 17395, A	Sequence 2113, Ap	Sequence 8030, Ap	12,	Sequence 12, Appl	Sequence 695, App	Sequence 1, Appl	Sequence 2, Appl	Sequence 1, Appl	Sequence 1, Appl	e 1	sequence /, Appli

ALIGNMENTS

RESULT 1 US-08-864-357F-9

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Sequence 9, Application US/08864357F

Patent No. 6255281

GENERAL INFORMATION:

APPLICANT: Claragen, Inc. & NIH

ITILE OF INVENTION: Use of Recombinant Huma

ITILE OF INVENTION: Fibrotic Conditions

ITILE OF INVENTION NUMBER: US/08/864,357F

CURRENT APPLICATION NUMBER: US/08/864,357F

CURRENT ETLING DATE: 1997-05-28

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.0

SEQ ID NO 9

LENGTH: 37

Type: Num
; FEATURE:
; OTHER INFORMATION: primer sequence US-08-864-357F-10
                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
ITILE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammator
ITILE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
                                                        SOFTWARE: Patentin ve
SEQ ID NO 10
LENGTH: 60
TYPE: DNA
CRGANIEM: artificial
                                                                                                                                                                                                                                                                                                                                                                   US-08-864-357F-10/c; Sequence 10, Application US/08864357F; Patent No. 6255281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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37; Conserv
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100.0%; Pred. No. 2.2e-12;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/234,245
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: US 60/071,878
EARLIER FILING DATE: 1998-01-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3715
TYPE: DNA
ORGANISM: Mus musculus
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Best Local
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Patent No. 6509457
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APPLICANT: Thomas Jefferson University
APPLICANT: Raphael Rubin
APPLICANT: Manorama Tewari
TITLE OF INVENTION: Compositions And Methods For Modulating
TITLE OF INVENTION: Apoptosis
FILE REFERENCE: TJU-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICATION NUMBER: US/08/760,534:
FILING DATE: 02-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,186
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JALKANEN, MARKKU
APPLICANT: JAAKKOLA, PANU
APPLICANT: VIHINEN, TAPANI
TITLE OF INVENTION: SYNDECAN ENHANCER ELEMENT AND SYNDECAN
TITLE OF INVENTION: STIMULATION OF CELLULAR DIFFERENTIATION
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                WASHINGTON
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                                                                                                   NUMBER: US/08/760,534A
02-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-760-534A-5
                             INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 233 base pairs
TENGTH: 700-161c acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09336757 Patent No. 6492344
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APPLICANT: JALKANEN, MARKKU
APPLICANT: VIAKKOLA, PANU
APPLICANT: VIHINEN, TAPANI
TITLE OF INVENTION: SYNDECAN ENHANCER ELEMENT AND SYNDECAN
TITLE OF INVENTION: STRUCLATION OF CELLULAR DIFFERENTIATION
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIF: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,8
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                           FILING DATE: 01-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: I
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                          REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
            LENGTH: 283 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGTCTAGCCTGT 28
                                                                                                             S: (202)
(202) 37
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linear
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordro, J.Y.
APPLICANT: Glordro, J.Y.
FILE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 12461
DM SEQ ID NO 12461
LENGTH: 422
TYDE: DNA
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Best Local S
Matches 14
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Patent No. 6639063
GENERAL INFORMATION:
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SOFTWARE: Patent.pm
SEQ ID NO 3565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ducdert, A.
APPLICANT: Ducdert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
                                                   Matches
                                                                       Query Match
Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                               TYPE: DNA
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LOCATION: 22..339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watch 37.8%; Score 14; DB 4; Length 341; Local Similarity 100.0%; Pred. No. 43;
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                   20 CTAGCCTGTGCAAC 33
                                                   14;
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37.8%; Score 14; DB 4; Length 422; ilarity 100.0%; Pred. No. 43; Conservative 0; Mismatches 0; Indels
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                                                                                                             Query Match
                                                                                            Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5703221ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIR
TITLE OF INVENTION: AND RELATED VACCINES
                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA: including PRIOR APPLICATION DATA: including PRIOR APPLICATION DATA: described PRIOR APPLICATION NUMBER: 08/157,811
                                                                                                                                                             FEATURE:
OTHER INFORMATION:
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STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                            LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                             TOPOLOGY: linear
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310 TCTÁGCCTGTGCÁÁ 323
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                                   19 TCTAGCCTGTGCAA 32
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                                                                                              Similarity
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JENTION: ISOLATED STEALTH VIRUSES
                                                                           Conservative
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                                                                       37.8%; Score 14; DB 1; 100.0%; Pred. No. 43; tive 0; Mismatches
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                                                                                                               Length 553;
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RESULT 5 - 388-26 US-08-465-388-26 Application US/08465388 Sequence 26, Application US/08465388 Patent No. 5753488

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GENERAL INFORMATION:

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US-08-463-115-18
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TRLERA: 67-3510
TRLEX: 67-3510
INFORMATION FOR SEQ ID NO: 26-
SEQUENCE CHARACTERISTICS:
LENGTH: 553 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                              Patent No.
        GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                Sequence 18, Application US/08463115 Patent No. 5703221
                                                                                                                                                                                                                                                                                                                                                                                  Matches
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PRIOR APPLICATION DATA: Including application PRIOR APPLICATION DATA: Including application PRIOR APPLICATION DATA: described below: APPLICATION NUMBER: 08/157,811

FILING DATE: No. 5753488ember 23, 1993
APPLICATION NUMBER: 07/687,502

FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
APPLICATION NUMBER: 07/763,039
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OTHER INFORMATION:
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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                                                                                                                                                                                                                                                                                                                                                                                                     Local
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  STREET: Suite 4700
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                                                                                                                                                                                                                                                                                                    310 TCTAGCCTGTGCAA 323
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633 West Fifth Street
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TVENTION: ISOLATED STEALTH VIR
TVENTION: AND RELATED VACCINES
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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ER: 213/300
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US-08-465-388-18
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                                                                                                                                                                                                                                                                                                Sequence 18, Applicat Patent No. 5753488
GENERAL INFORMATION:
APPLICANT: WILLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION:
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                         STREET:
STREET:
CITY: L
COMPUTER:
                                                                               COUNTRY: U.S.A. ZIP: 90071-2066
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FILING DATE: MAY 23, 1995

FILING DATE: MAY 25

PRIOR APPLICATION DATA: including application prior. APPLICATION DATA: including application prior. APPLICATION DATA: described below: APPLICATION NUMBER: 08/157,811

FILING DATE: No. 5703221ember 23, 1993

APPLICATION NUMBER: 07/887,502

FILING DATE: MAY 23, 1991

APPLICATION NUMBER: 07/704,814

FILING DATE: MAY 23, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: September 20, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: September 20, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: MAY 23, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: MAY 23, 1991

APPLICATION NUMBER: 07/763,039
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SEQUENCE CHARACTERISTICS:
LENGTH: 715 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                   APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSeq Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                          STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (213) 955-0440
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FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 TCTÁGCCTGTGCÁÁ 338
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                                                                                                                                                                                                                E: Lyon & Lyon
633 West Fifth Street
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IBM Compatible
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OPERATING SYSTEM:

IBM P.C. DOS 5.0

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                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR RELING DATE: 1998-02-18
PRIOR REPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-727
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5999
LENGTH: 1374
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 715 harmone
                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5999, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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FILING DATE: No. 5753488ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
APPLICATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELEZHONE: (213) 489-1600
TELEZHONE: (213) 489-1600
                                                                                    Matches
                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-160
TELEFAX: (213) 955-0440
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78
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                                                                                    14; Conservative
                                      4 GAGAAGATCGCTCA 17
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                                                                                                       Similarity
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                                                                               37.8%; Score 14;
100.0%; Pred. No.
tive 0; Mismatc
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                                                                                    Mismatches
                                                                                                    DB 4; Length 1374; 43;
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US-08-465-388-2
Sequence 2. Application US/08465388
Patent No. 5753488
GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: AND RELATED VACCINES
TITLE OF INVENTION: AND RELATED VACCINES
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US-08-463-115-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1540 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Patent No. 5703221
GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
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APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/301
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: IBM P.C. DOS!
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,1:
FILING DATE: June 5, 1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA: including
PRIOR APPLICATION DATA: described
DEFINATION DATA: described
DEFINATION DATA: described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5703221ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
ETITION DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
                                                                                                                                                                                                                                                                                                                                           Local
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Los Angeles
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                                                                                                                                                                                                                                                                                                                        Conservative
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NUMBER OF SEQUENCES: 1

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US-09-252-991A-6306
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Sequence 6306, Application US/09252991A
Patent No. 6551795
GENERRAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6306
LENGTH: 1899
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CURRENT APPLICATION NUMBER: US/08/465,388

FILING DATE: June 5,1995

FILING DATE: June 5,1995

PRIOR APPLICATION DATA: including application prior Application DATA: including application prior Application DATA: described below: APPLICATION NUMBER: 09/157,811

FILING DATE: No. 575348ember 23, 1993

APPLICATION NUMBER: 07/887,502

FILING DATE: May 22, 1992

APPLICATION NUMBER: 07/704,814

FILING DATE: May 23, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: September 20, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: September 20, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: September 20, 1991

APPLICATION NUMBER: 07/763,039
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1540 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             997 TCTAGCCTGTGCAA 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 37.8%; Score 14; DB 1; Length 1540; l Similarity 100.0%; Pred. No. 43; 14; Conservative 0; Mismatches 0; Indels
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ER: 213/300
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; TYPE: DNA;
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6306

Query Match
Query Match
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps
Matches 14; Conservative 17

Qy 4 GAGAAGATCGCTCA 17
Db 1534 GAGAAGATCGCTCA 1547
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Search completed: December 23, 2004, 01:33:53
Job time: 40.8009 secs

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Database :
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_EUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
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Gapop_60.0 , Gapext 60.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 12	c 11	c 10	ω	ი 8	c 7	ი ი	c 5	4	ω	N	1	Result No.
15	15	16	16	37	37	37	37	37	37	37	37	Score
40.5	40.5	43.2	43.2	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query
389	261	78268	32706	60	60	60	60	37	37	37	37	Query Match Length DB
16	18	13	13	16	15	10	9	16	15	10	9	DB
US-10-424-599-75149	US-10-674-124A-5867	US-10-087-192-742	US-10-087-192-1750	US-10-647-371-9	US-10-187-498A-5	US-09-898-616A-5	US-09-861-688-10	US-10-647-371-8	US-10-187-498A-4	US-09-898-616A-4	US-09-861-688-9	HD
Sequence 75149, A	Sequence 5867, Ap	Sequence 742, App	Sequence 1750, Ap	Sequence 9, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 10, Appl	Sequence 8, Appli	Sequence 4, Appli		Sequence 9, Appli	Description

RESULT 2 US-09-898-616A-4

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-	-09-791-2	-10-437-963-948	-10-437-963-4701	-10-437-963-9485	-10-437-963-9484	-10-437-963-9484	-10-437-963-9483	-10-437-963-4700	-10-437-963-9477	-10-437-963-9480	-10-437-963-9476	-10-437-963-4700	-10-437-963-9476	-10-437-963-9480	-10-437-963-	-10-437-963-9480	-10-437-963-9485	-09-791-254-	-767-701-1489	-10-437-963-4	-10-437-963-9484	-10-799-747-2	-10-195-730-	-10-653-595-8	-09-397-945-8	-10-425-115-9018	-10-424-599-1099	-10-424-599-826	-10-027-632-13178	-10-027-632-13178	-10-027-632-1317	-10-027-632-13178	18-995-131
	equence 1, Appl	equence 94812,	equence 47011,	equence 94855,	equence 94841,	equence 94843,	equence 94836,	equence 47002,	equence 94774,	equence 94802,	equence 94769,	equence 47007,	equence 94766,	equence 94807,	equence 94776,	equence 94806,	equence 94851,	equence 4, Appl	equence 1489	equence 46992,	equence 94846,	equence 20, Api	equence 20, App	equence 82, App	equence 82, App	equence 90184,	equence 1099	equence 8265	equence 1317	equence 1317	equence 1317	quence 131785,	equence 1312

AL IGNMENTS

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; LENGTH: 37
; TYPE: DNA
; CRGANISM: Artificial Sequence
; FEATURE:
; CTHER INFORMATION: primer sequence
US-09-861-688-9
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US-09-861-688-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09861688; Patent No. US20020173460A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of
TITLE OF INVENTION: Inflammatory and
TITLE OF INVENTION: Pibrotic Conditions
FILE REPERBICE: 116142/2
CURRENT APPLICATION NUMBER: US/09/861,688
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: U8/864,357
PRIOR APPLICATION NUMBER: 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
                                                                                            Matches
                                                                                                                                           Query Match
                                                                                                                   Best Local
                               1 ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 37
                                                                                            37; Conservative
1 ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 37
                                                                                                              h 100.0%; Score 37; DB 9; Length 37; Similarity 100.0%; Pred. No. 1.3e-12;
                                                                                         0;
                                                                                            Mismatches
                                                                                         ;
                                                                                         Gaps
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ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 37

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US-10-187-498A-4
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Best Local S
Matches 37
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CURRENT APPLICATION NUMBER: US/09/898,616A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                 Matches
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APPLICANT: Claragen Inc.
APPLICANT: Pilon, Aprile L
APPLICANT: Pilon, Aprile L
APPLICANT: Walch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment of TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09898616A
Publication No. US20030109429A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Clarage Inc.
APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Wethod for the Production of Purified rhUG for the Treatment
TITLE OF INVENTION: Imflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00260
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR PRIOR DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Publication No. US20030207795A1
                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
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OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 37
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                                                                                                       Local
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                            1 ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 37
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                                                                                                       h 100.0%; Score 37; DB 15; Similarity 100.0%; Pred. No. 1.3e-12;
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Conservative
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                                                                                 0; Mismatches
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                                                                                                                              Length 37,
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; Sequence 5, Application US/09898616A ; Publication No. US20030109429A1 ; GENERAL INFORMATION:
                                                                        US-09-898-616A-5/c
                                                                                                 RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: primer sequence US-10-647-371-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-861-688-10/c
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Publication No. US20040047857A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09861688
Patent No. US20020173460A1
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                        Query Match
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of
TITLE OF INVENTION: Inflammatory and
TITLE OF INVENTION: Fibrotic Conditions
FILE OF INVENTION CONDITIONS
FILE OF INVENTION NUMBER: US/09/861,688
CURRENT APPLICATION NUMBER: US/09/861,688
CURRENT FILING DATE: 2001-05-21
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory
TITLE OF INVENTION: and Fibrotic Conditions
FILE REFERENCE: 116142-85
CURRENT APPLICATION NUMBER: US/10/647,371
CURRENT FILING DATE: 2003-08-25
PRIOR APPLICATION NUMBER: 09/549,926
PRIOR APPLICATION NUMBER: 09/549,926
PRIOR PILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: primer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                            37 ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 1
                                                                                                                                                                                                                                                                        l Similarity 100.
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 37; DB 16; l Similarity 100.0%; Pred. No. 1.3e-12; 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                    1 ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 37
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                                                                                                                                                                                                                                                                                             100.0%; Score 37; DB 9; 100.0%; Pred. No. 1.3e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 60
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SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 60
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Best Local
                                                                                                                                            Matches
                                                                                                                                                            Query Match
Best Local
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APPLICANT: Welch, Richard W
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment (
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00170
CURRENT APPLICATION NUMBER: US/09/898,616A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ. ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pilon, Aprile L
APPLICANT: Welch, Richard W
TITLE OF INVENTION: Method for the Production of Purified rhUG for the Treatment
TITLE OF INVENTION: Inflammatory and Fibrotic Conditions
FILE REFERENCE: 116142/00260
CURRENT APPLICATION NUMBER: US/10/187,498A
CURRENT FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US 08/864,357
PRIOR FILING DATE: 1997-05-28
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APPLICANT: Pilon, Apri
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OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
OTHER INFORMATION: Original amino acid sequence obtained from cDNA.
OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Original amino acid sequence obtained from cDNA. OTHER INFORMATION: d sequence maximized for expression in E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                     FEATURE
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                                                                                                                                         37;
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                                                                                           1 ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 37
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                                                 ATGGAGAAGATCGCTCAGTCTAGCCTGTGCAACTAAG 1
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                                                                                                                                                            100.0%; Score 37; DB 15; 100.0%; Pred. No. 1.3e-12;
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APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
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RESULT 10
US-10-087-192-742/c
US-10-087-192-742/c
; Sequence 742, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
CONTRACTION:
David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ 1D NOS: 2059
NUMBER OF SEQ 1D NOS: 2059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Description of Artificial Sequence: primer sequence US-10-647-371-9
                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-10-087-192-1750
                                                                                                                                                                                   밁
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APPLICANT: Claragen, Inc. & NIH; TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatory, TITLE OF INVENTION: and Fibrotic Conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1750, Application US/10087192 Publication No. US20020182586A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1750
LENGTH: 32706
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/647,371
CURRENT FILING DATE: 2003-08-25
PRIOR APPLICATION NUMBER: 09/549,926
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEO ID NOS: 12
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Morris, David W. APPLICANT: Engelhard, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 60
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                     7293 TCTAGCCTGTGCAACT 7308
                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                19 TCTAGCCTGTGCAACT 34
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100.0%; Pred. No. 1.3e-12;
                                                                                                                                                                                                                                                                                                 43.2%; Score 16; DB 13; Length 32706; 100.0%; Pred. No. 7.4;
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CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2059
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 742
SEQ ID NO 742
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US-10-674-124A-5867/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP2002-383869
PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 27110
SEQ ID NO 5867
                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5867, Application US/10674124A Publication No. US20040197797A1 GENERAL INFORMATION:
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                                                                                                Matches
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PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: JP2000-112699
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: JP2002-327516
PRIOR ETITION NUMBER: JP2002-327516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: INOKO, Hidetoshi
APPLICANT: TAMIVA, Gen
TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE.
TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
FILE REFERENCE: ORIN-003CIP
CURRENT APPLICATION NUMBER: US/10/674,124A
CURRENT FILING DATE: 2003-09-26
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PRIOR FILING DATE: 2003-03-07
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                                                                                                                                                                                                              OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and OTHER INFORMATION: 5'-terminus of this base sequence: 130675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: chromosomal short are OTHER INFORMATION: sequence: 147898939
                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Distance between a terminus base of telomere on OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: AC072028.5_149909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 261
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                                                                                                                     local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION: Located on chromosome 3
                                              19 тстассстстская зз
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                                                                                                15;
                                                                                                Conservative
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                                                                                   40.5%; Er
100.0%; Er
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                                                                                                                  Score 15; DB 18; Length 261; Pred. No. 36;
                                                                                                Mismatches
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                                                                                                Indels
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                                                                                             Gaps
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APPLICANT: Hyseq, inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1312
LENGTH: 477
TYPEN: NAN
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US-09-918-995-1312
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RESULT 14
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Publication No. US20040031072A1

GENERAL IMPORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Cabo Yihua

APPLICANT: Cabo Yihua

APPLICANT: Cabo Yongwei

TITLB OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLB OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

FULR REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 75149

LENGTH: 389

TYPER: NAM
                                                                                                                                                           Query Match
Best Local S
Matches 15
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Publication No. US20030073623A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
FEATURE;
NAME/KBY: misc_feature
LOCATION: (1)...(477)
OTHER INFORMATION: n = A,T,C or G
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FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_38873C.1
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                    Local Similarity
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                                                                      305 TGGAGAAGATCGCTC 319
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                                                                                                                                                              40.5%; Score 15; DB 10;
100.0%; Pred. No. 35;
tive 0; Mismatches 0
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                                                                                                                                                                                                           Length 477;
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US-10-027-632-131785/c
; Sequence 131785, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:

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PRIOR APPLICATION NUMBER: US 60/18,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR PILICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PSSESED for Windows Version 4.0
SEQ ID NO 131786
LENGTH: 574
TYPE: DNA
ORGANISM: Human
US-10-027-632-131786
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PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER: US 60/146,002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131785
LENGTH: 574
TYPE: DNA
ORGANISM: Human
US-10-027-632-131785
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US-10-027-632-131786/c
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,363
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
      Matches
                                 Query Match
Best Local Similarity
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FILE REFERENCE: 108827.129
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         15;
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      Conservative
40.5%; Score 15; DB 13; Length 574; 100.0%; Pred. No. 35; ative 0; Mismatches 0; Indels
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Search completed: December 23, 2004, 05:19:30 Job time : 520.67 secs

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